

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 12:30:01 / Search time 15657 Seconds
(without alignments)
11505.199 Million cell updates/sec

Title: US-10-792-307-3

Perfect score: 3169

Sequence: 1 gcagctgctgctgaccatgag.....atttcacatccagaggaag 3169

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 110

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database :

GenEmbl: +
1: gb_ba: +
2: gb_in: +
3: gb_env: +
4: gb_cm: +
5: gb_ov: +
6: gb_pat: +
7: gb_ph: +
8: gb_pr: +
9: gb_ro: +
10: gb_sta: +
11: gb_sy: +
12: gb_uni: +
13: gb_vl: +
14: gb_hig: +
15: gb_pl: +

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------------|--------------------|
| 1 | 3169 | 100.0 | 3169 | 8 AF417580 | AF417580 Homo sapi |
| 2 | 602 | 19.0 | 159272 | 8 HSDJ686C3 | AL049712 Human DNA |

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|---|-----|------|--------|--------------|--------------------|
| 3 | 493 | 15.6 | 2560 | 6 AX833218 | AX833218 Sequence |
| 4 | 493 | 15.6 | 2560 | 8 AK094789 | AK094789 Homo sapi |
| 5 | 308 | 9.7 | 3566 | 6 CQ850588 | CQ850588 Sequence |
| 6 | 308 | 9.7 | 3566 | 8 AK127751 | AK127751 Homo sapi |
| 7 | 298 | 9.4 | 884 | 6 CQ728483 | CQ728483 Sequence |
| 8 | 144 | 4.5 | 321519 | 14 AL714004 | AL714004 Homo sapi |
| 9 | 116 | 3.7 | 635 | 10 HS692H20T | AL034506 H.sapiens |

ALIGNMENTS

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DEFINITION Homo sapiens transmembrane channel-like protein 2 (TMCC2) mRNA,
complete cds.
ACCESSION AF417580
VERSION AF417580.2 GI:28642834
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 3169)
Kurima,K., Peters,L.M., Yang,Y., Riazuddin,S., Ahmed,Z.M., Naz,S.,
Arnud,D., Drury,S., Mo,J., Makshima,T., Ghosh,M., Menon,P.S.N.,
Dehnmukh,D., Oddoux,C., Ostroff,H., Khan,S., Riazuddin,S.,
Dehnmukh,P.L., Hampton,L.V., Sullivan,S.L., Battey,J.F.,
Keats,B.J.B., Wilcox,E.R., Friedman,T.B. and Griffith,A.J.
Dominant and recessive deafness caused by mutations of a novel
gene, TMCC1, required for cochlear hair-cell function
Nat. Genet. 30 (3), 277-284 (2002)
11850618
2 (bases 1 to 3169)
Kurima,K., Griffith,A.J. and Friedman,T.B.
Direct Submission
Submitted (10-SEP-2001) NIDCD, NIH, 5 Research Court, #2A02,
Rockville, MD 20850, USA
3 (bases 1 to 3169)
Kurima,K., Griffith,A.J. and Friedman,T.B.
Direct Submission
Submitted (03-MAR-2003) NIDCD, NIH, 5 Research Court, #2A02,
Rockville, MD 20850, USA
Sequence update by submitter
On Mar 3, 2003 this sequence version replaced gi:19223982.
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FEATURES
source

gene

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ORIGIN

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RESULT 2
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LOCUS
DEFINITION
HSDJ686C3 159272 bp DNA linear Pri 18-MAY-2005
Human DNA sequence from clone RP4-686C3 on chromosome 20. Contains
the IDH3B gene for isocitrate dehydrogenase 3 (NAD⁺) beta, the
NOL5A gene for nucleolar protein 5A (56kDa with KKE/D repeat), the
TMC2 gene for transmembrane cochlear expressed protein 2, a novel
gene, the RNUS6 gene for small nuclear RNA U56, the RNUS7 gene for
small nuclear RNA U57, the 5' end of one variant of the ZNF343 gene
for zinc finger protein 343 and three Opc islands, complete
sequence.

ACCESSION
VERSION
KEYWORDS
AL049712.12 GI:5629919
HTG; C20orf145; OPG Island; FLJ37470; IDH3B; Isocitrate
dehydrogenase 3; NOL5A; NOP56; nucleolar protein 5A; RNUS6; RNUS7;
small nuclear RNA; TMC2; ZNF343.

SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 159272)

REFERENCE
AUTHORS
TITLE
JOURNAL
Smith, M.
Direct Submision
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
Clone requests: clonerequests@sanger.ac.uk
On Jul 28, 1999, this sequence version replaced gi:5578962.

COMMENT
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Emi; EMBL; Swi; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone compigs of human
chromosome 20, constructed by the Sanger Centre Chromosome 20
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr20
RP4-686C3 is from the library RPCI-4 constructed by the group of
Pleier de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC

FEATURES
source
Web site: <http://www.sanger.ac.uk>
Contact: vegas@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one subclone; and the assembly was confirmed by restriction digest,
except on the rare occasion of the clone being a YAC.
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 11773..11919,12156..12250,12364..12424,13112..13190,
 13427..13555)
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 /note="match: ESTs: AA94485 BE967093 BF967981 BF978210

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 VIREQTEGEVSSLEHESARGVIECLKIVTAKSQRIARFAVDATPKGKGVAVHK
 ANIMRLGGDLFLQCCIEVALYPRKIFETMIDNCCQAVQNPQDFVLMNLYGNI
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 join(7761..7796,7944..8024,8191..8289,8383..8503,
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 13427..13440)
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 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 652; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2517 AGAGACCACTCTCCTCTGCGACGCAAGCGCATGGACACAGAGCGCGCGCC 2576
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 DB 30817 AGAGACCACTCTCCTCTGCGACGCAAGCGCATGGACACAGAGCGCGCGCC 30758
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 QY 2577 TGGAGCTCCATCTGCGACGAGGACCACTGCTGCTGCGACCTTCTATATC 2636
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 DB 30757 TGGAGCTCCATCTGCGACGAGGACCACTGCTGCTGCGACCTTCTATATC 30698
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QY 2637 TCAGCCCCCTGGAATCGGACCAAGATTCTGGCCAGGCCCACTCTCAACTCATCCGTGAG 2696
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Db 30637 CTCAGCCTCTGGAAAAGTGTCTAGAGACCTCCCACTGAGGGTGAAGCTCCAGGGAC 30578
QY 2757 CTCAGCCTAGGGCTGATCCTCAAGTACCCAGTTTCACACATACCAACCAAGTTCTC 2816
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Db 30577 CTCAGCCTAGGGCTGATCCTCAAGTACCCAGTTTCACACATACCAACCAAGTTCTC 30518
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Db 30397 GAAGCTGAAGCCTCTCTGCACTAACTGCCCCCTCCCAATATCTTGGTTCAGACAGCTCTG 30338
QY 2997 AACCCACGCTCAACAGTGTGCACTTGGCTCCGATTTTGGAGTTGGGAGAGGCCAT 3056
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Db 30277 GACCAAGCTGTGAGACTTTTCCATGGGATCAAGTTTAGAGACAGGGTTTCTGCCACTT 30218
QY 3117 CCTTAACAGAGAGGGGATGAGAGAGGGCTACATTTCTCAATCCAGAGGAAG 3169
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RESULT 3
AX833218 2560 bp DNA linear PAT 15-DEC-2003
LOCUS Sequence 342 from Patent EP1347046.
DEFINITION AX833218
ACCESSION AX833218
VERSION AX833218.1 GI:39919353
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nageharu,K. and
Masuko,Y.
Full-length cDNA sequences
Patent: EP 1347046-A 342 24-SEP-2003;
Research Association for Biotechnology (JP)

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Best Local Similarity 99.7%; Pred. No. 7e-272;
Matches 593; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1473 GTTGAAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1532
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Db 181 GTTGAAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 1533 GGGACGCACTTTGCACTCTTCTGCGGAACTCTACACATTTCTCTTGGCCCTGATGGA 1592
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Db 301 TGACGTCACTCAAGCTTGTCTAATGAAAGACATTAAGACATCACTCACTGCACTCT 360
QY 1653 GTTTAATATTACAACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1712
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Db 361 GTTTAATATTACAACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
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RESULT 4
AX094789 2560 bp mRNA linear PRI 30-JAN-2004
LOCUS Homo sapiens cDNA FLJ37470 f1s, clone BRAHM201258.
DEFINITION AX094789
ACCESSION AK094789

| | |
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| VERSION | AK094789.1 GI:21753918 |
| KEYWORDS | oligo capping; fis (full insert sequence). |
| SOURCE | Homo sapiens (human) |
| ORGANISM | Homo sapiens |
| REFERENCE | Eukaryote; Metazoa; Chordata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo. |
| AUTHORS | Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Matite, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosori, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsura, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ichibashi, T., Yamashita, H., Murekawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hirooka, S., Chiba, Y., Ishide, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Houta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shionawa, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hiroo, M., Omori, Y., Kambara, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsunaga, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togaishi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. |
| TITLE | Complete sequencing and characterization of 21,243 full-length human cDNAs |
| JOURNAL | Nat. genet. 36 (1), 40-45 (2004) |
| PUBMED | 14702039 |
| REFERENCE | |
| AUTHORS | 2 Suzuki, O., Sasaki, N., Aotsuka, S., Shoji, T., Ichihara, T., Shiohata, N., Matsumoto, K., Hirano, M., Sano, S., Nomura, R., Yoshikawa, Y., Matsumoto, K., Moriye, S., Chiba, E., Momiyama, H., Onogawa, S., Kaeriyama, S., Satoh, N., Matsunawa, H., Takahashi, E., Katoke, R., Kuga, N., Kuroda, A., Satoh, I., Kamata, K., Takami, S., Terashima, Y., Watanabe, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai, H., O, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakami, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T. |
| TITLE | NEDO human cDNA sequencing project |
| JOURNAL | Unpublished |
| REFERENCE | 3 (bases 1 to 2560) |

| | |
|-----------------------|--|
| AUTHORS | Isogai, T. and Yamamoto, J. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kametari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) |
| COMMENT | NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB. |
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| | /tissue_type="brain" |
| | /clone_id="BRAM2" |
| | /note="cloning vector: pME185FL3" |
| | 104..721 |
| CDS | /note="unnamed protein product" |
| | /codon_start=1 |
| | /protein_id="BAC04423.1" |
| | /db_xref="GI:21753919" |
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| Best Local Similarity | 99.7%; Pred. No. 7e-272; |
| Matches | 593; Conservative 0; Mismatches 2; Indels 0; Gaps 0; |
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| DB | 1 AAGATTTCTTCTGTCCTGGCCAACTTCTCATCTGCTGTTGTGTGGAACTGGGTA 60 |
| QY | 1353 CCTCATTTACTTGGTGAAGCATCTCAAGCAATTCGAAAAATCGAAGTCTGAGCTG 1412 |
| DB | 61 CCTCATTTACTTGGTGAAGCATCTCAAGCAATTCGAAAAATCGAAGTCTGAGCTG 120 |
| QY | 1413 GTATGAAGGATGAGGTAGAGATGATGTCCTGCTTGAATGTTTGTCCCTCT 1472 |
| DB | 121 GTATGAAGGATGAGGTAGAGATGATGTCCTGCTTGAATGTTTGTCCCTCT 180 |
| QY | 1473 GTTTGAACCATGCTGCTGGAGATTAACACCCACGACGACGACGAGAGTGGCAGCT 1532 |
| DB | 181 GTTTGAACCATGCTGCTGGAGATTAACACCCACGACGACGACGAGAGTGGCAGCT 240 |
| QY | 1533 GGAAGCATTTGACGCTTCTGCGGGAACCTACACATTTCTGTGGCCCTGATGGA 1592 |
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LK"
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Best Local Similarity 100.0%; Pred.No. 5.4e-165;
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 163 CCTCATATGCTGAGTTTGATATTATGGAATGTGCTGGTTTGATCTTCAACCAAGA 222
QY 1948 ATGATCTGAGTGGGCTCCTTCTATGCTCAAGGCTGGTGGCATTAAATGTGCTGGCCTG 2007
DB 223 ATGATCTGAGTGGGCTCCTTCTATGCTCAAGGCTGGTGGCATTAAATGTGCTGGCCTG 282
QY 2008 CTGAGCTTCATGTACTCAATGCTGGGGGTGATGAGGCAAGTACCCATGAAAGC 2067
DB 283 CTGAGCTTCATGTACTCAATGCTGGGGGTGATGAGGCAAGTACCCATGAAAGC 342
QY 2068 GTGTTCAAGGCTCCCGATCCCAAACTTCTACATGGGCTCTGCTGGTGGTCTTC 2127
DB 343 GTGTTCAAGGCTCCCGATCCCAAACTTCTACATGGGCTCTGCTGGTGGTCTTC 402
QY 2128 CTCAGGCTCCTGCCGGTGGCTACACATCATGTCCCTCCACCCCTCTTTGACTGGGG 2187
DB 403 CTCAGGCTCCTGCCGGTGGCTACACATCATGTCCCTCCACCCCTCTTTGACTGGGG 462
QY 2188 CGGTCAAG 2195
DB 463 CGGTCAAG 470
RESULT 7
LOCUS CQ728483 884 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 14417 from Patent WO02068579.
ACCESSION CQ728483
VERSION CQ728483.1 GI:42297418

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kitz, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 14417 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
ORIGIN
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Best Local Similarity 100.0%; Pred.No. 3e-159;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 946 GAGGGCTATATCAAGTACTGCTGCTCTGCTATGCTACTACAAACCAAGGACCATC 1005
DB 187 GAGGGCTATATCAAGTACTGCTGCTCTGCTATGCTACTACAAACCAAGGACCATC 246
QY 1006 GGGTGGCTAGGATACCGGCTGCTTATGCTTATGCTGGGGGTACGGGTCTTGCGC 1065
DB 247 GGGTGGCTAGGATACCGGCTGCTTATGCTTATGCTGGGGGTACGGGTCTTGCGC 306
QY 1066 TACAGCTGATATTGTTCATTCGATCGATGGCCAGCAATACCAAGAAAGCAGGCGAA 1125
DB 307 TACAGCTGATATTGTTCATTCGATCGATGGCCAGCAATACCAAGAAAGCAGGCGAA 366
QY 1126 GGGGAGGTGACACATTCACATTACGCTTCAGAGTGTTCACAGCTGGGACTACTGATC 1185
DB 367 GGGGAGGTGACACATTCACATTACGCTTCAGAGTGTTCACAGCTGGGACTACTGATC 426
QY 1186 GGGAAATCAGAGACAGCTGATTAACAAATATGATTCATCACACAGCTTCAGAGAA 1243
DB 427 GGGAAATCAGAGACAGCTGATTAACAAATATGATTCATCACACAGCTTCAGAGAA 484
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DEFINITION Homo sapiens clone XX-CR_20-17119-3, *** SEQUENCING IN PROGRESS
***, 89 unordered pieces.
ACCESSION AL714004
VERSION AL714004.35 GI:21104209
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

Hominidae; Homo.
1 (bases 1 to 321519)
Plumb, B.
Direct Submission
Submitted (20-MAY-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 22, 2002 this sequence version replaced gi:21068608.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: Chr 20-17119-3
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 254683 bases at least Q40
Consensus quality: 281730 bases at least Q30
Consensus quality: 299177 bases at least Q20
Insert size: 312719; sum-of-contigs
Quality coverage: 1.63x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 89 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 4746: contig of 4746 bp in length
* 4747 4846: gap of 100 bp
* 4847 7172: contig of 2326 bp in length
* 7173 7272: gap of 100 bp
* 7273 9289: contig of 2017 bp in length
* 9290 9389: gap of 100 bp
* 9390 11807: contig of 2418 bp in length
* 11808 11907: gap of 100 bp
* 11908 13962: contig of 2055 bp in length
* 13963 14062: gap of 100 bp
* 14063 16347: contig of 2285 bp in length
* 16348 16447: gap of 100 bp
* 16448 18532: contig of 2085 bp in length
* 18533 18632: gap of 100 bp
* 18633 20654: contig of 2022 bp in length
* 20655 23021: gap of 100 bp
* 23022 23121: contig of 2267 bp in length
* 23122 25134: gap of 100 bp
* 25135 25234: contig of 2013 bp in length
* 25235 28285: gap of 100 bp
* 28286 28385: contig of 3051 bp in length
* 28386 30542: gap of 100 bp
* 30543 30642: contig of 2157 bp in length
*
30643 33433: contig of 2791 bp in length
* 33434 33533: gap of 100 bp
* 33534 35599: contig of 2066 bp in length
* 35600 35699: gap of 100 bp
* 35700 39866: contig of 4167 bp in length
* 39867 39966: gap of 100 bp
* 39967 50793: contig of 10833 bp in length
* 50800 50899: gap of 100 bp
* 50900 55372: contig of 4473 bp in length
* 55373 55472: gap of 100 bp
* 55473 58398: contig of 2926 bp in length
* 58399 58498: gap of 100 bp
* 58499 61834: contig of 3336 bp in length
* 61835 72530: gap of 100 bp
* 72531 72630: contig of 10596 bp in length
* 72631 77693: gap of 100 bp
* 77693 77793: contig of 5065 bp in length
* 77793 77996: gap of 100 bp
* 77996 80590: contig of 2793 bp in length
* 80591 80690: gap of 100 bp
* 80691 85052: contig of 4362 bp in length
* 85053 85152: gap of 100 bp
* 85153 89287: contig of 4135 bp in length
* 89288 89387: gap of 100 bp
* 89388 91654: contig of 2267 bp in length
* 91655 91754: gap of 100 bp
* 91755 94398: contig of 2644 bp in length
* 94399 94498: gap of 100 bp
* 94499 96771: contig of 2273 bp in length
* 96772 96871: gap of 100 bp
* 96872 103634: contig of 6763 bp in length
* 103635 103734: gap of 100 bp
* 103735 107935: contig of 4201 bp in length
* 107936 108035: gap of 100 bp
* 108036 113903: contig of 5868 bp in length
* 113904 114003: gap of 100 bp
* 114004 116208: contig of 2205 bp in length
* 116209 116308: gap of 100 bp
* 116309 118998: contig of 2690 bp in length
* 118999 119098: gap of 100 bp
* 119099 122033: contig of 2935 bp in length
* 122034 122133: gap of 100 bp
* 122134 124238: contig of 2105 bp in length
* 124239 124338: gap of 100 bp
* 124339 126514: contig of 2176 bp in length
* 126515 126614: gap of 100 bp
* 126615 136561: contig of 9947 bp in length
* 136562 136661: gap of 100 bp
* 136662 139137: contig of 2476 bp in length
* 139138 139237: gap of 100 bp
* 139238 142728: contig of 3491 bp in length
* 142729 142828: gap of 100 bp
* 142829 165779: contig of 22951 bp in length
* 165780 165879: gap of 100 bp
* 165880 168731: contig of 2852 bp in length
* 168732 168831: gap of 100 bp
* 168832 170924: contig of 2093 bp in length

170925 171024: gap of 100 bp
171025 173244: contig of 2220 bp in length
173245 173344: gap of 100 bp
173345 176010: contig of 2666 bp in length
176011 176110: gap of 100 bp
176111 178420: contig of 2310 bp in length
178421 178520: gap of 100 bp
178521 181160: contig of 2640 bp in length
181161 181260: gap of 100 bp
181261 184022: contig of 2762 bp in length
184023 184122: gap of 100 bp
184123 186233: contig of 2111 bp in length
186234 186333: gap of 100 bp
186334 188474: contig of 2141 bp in length
188475 188574: gap of 100 bp
188575 190834: contig of 2260 bp in length
190835 190934: gap of 100 bp
190935 193769: contig of 2835 bp in length
193770 193869: gap of 100 bp
193870 196119: contig of 2250 bp in length
196120 196219: gap of 100 bp
196220 200732: contig of 4513 bp in length
200733 200832: gap of 100 bp
200833 204093: contig of 3261 bp in length
204094 204193: gap of 100 bp
204194 206520: contig of 2327 bp in length
206521 206620: gap of 100 bp
206621 208679: contig of 2059 bp in length
208680 208779: gap of 100 bp
208780 210932: contig of 2153 bp in length
210933 211032: gap of 100 bp
211034 213133: contig of 2101 bp in length
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213234 217420: contig of 4187 bp in length
217421 217520: gap of 100 bp
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222146 222245: gap of 100 bp
222246 224782: contig of 2537 bp in length
224783 224882: gap of 100 bp
224883 227854: contig of 2972 bp in length
227855 227954: gap of 100 bp
227955 230320: contig of 2366 bp in length
230321 230420: gap of 100 bp
230421 232905: contig of 2485 bp in length
232906 233005: gap of 100 bp
233006 236533: contig of 3528 bp in length
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239253 239352: contig of 2619 bp in length
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239354 248789: contig of 9437 bp in length
248790 248889: gap of 100 bp
248890 250940: contig of 2051 bp in length
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253163 253262: gap of 100 bp
253263 253411: contig of 2149 bp in length
253412 255111: gap of 100 bp

255112 258118: contig of 2607 bp in length
258119 258218: gap of 100 bp
258219 260751: contig of 2533 bp in length
260752 260851: gap of 100 bp
260852 263142: contig of 2291 bp in length
263143 263242: gap of 100 bp
263243 263368: contig of 2126 bp in length
263369 265468: gap of 100 bp
265469 268121: contig of 2653 bp in length
268122 268221: gap of 100 bp
268222 270223: contig of 2002 bp in length
270224 270323: gap of 100 bp
270324 274441: contig of 4118 bp in length
274442 274541: gap of 100 bp
274542 276791: contig of 2250 bp in length
276792 276891: gap of 100 bp
276892 280982: contig of 4091 bp in length
280983 281082: gap of 100 bp
281083 283442: contig of 2360 bp in length

Query Match 4.5% Score 144; DB 14; Length 321519;
Best Local Similarity 99.5% Pred. No. 3.8e-70;

Matches 194; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1237 AAGGATCAATAGTGGATGAACAGAGATACAAAGAAATATCCATCTGACACAGA 1296
|||||
DB 317605 AAGGATCAATAGTGGATGAACAGAGATACAAAGAAATATCCATCTGACACAGA 317546

QY 1297 TTCTCTGTGTCTCTGCGCAACTTCTCATCATCTGCTGTTGTGTGAAGTGGTACTTC 1356
|||||
DB 317545 TTCTCTGTGTCTCTGCGCAACTTCTCATCATCTGCTGTTGTGTGAAGTGGTACTTC 317486

QY 1357 ATTACTTGTGTGAAGGATCTGAGCAATCTCCAAATGCGAATGTCAGCTGGTAT 1416
|||||
DB 317485 ATTACTTGTGTGAAGGATCTGAGCAATCTCCAAATGCGAATGTCAGCTGGTAT 317426

QY 1417 GAAGGATGAGGTA 1431
|||||
DB 317425 GAAGGATGAGGTA 317411

RESULT 9
H5692H20T
LOCUS H5692H20T 635 bp DNA linear STS 14-DEC-1998
DEFINITION H-sepiens STS from genomic clone 692H20, sequence tagged site.
ACCESSION AL034506
VERSION AL034506.1 GI:4008495
KEYWORDS STS, single read.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 635)

AUTHORS Delbukas, P., O'Neill, L., Holden, J., Mistry, D., Huckle, E., Taylor, R. and Hunt, S.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1998) E-mail contact: humquery@sanger.ac.uk
COMMENT Mariner std692H207 (Primer A : AATGAAGAGAGAAAGAGGG; Primer B : GGTAAGCTCAGAGCTGGTGG; amplicon size : 176 bp) is from sequence generated from the T7 end of PAC 692H20. 692H20 is part of the bacterial clone contigs constructed by the Chromosome 20 Mapping Group. (<http://www.sanger.ac.uk/HGP/Chr20/>) 692H20 is from the library RPC14 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong.

For further details see <http://bacpac.med.buffalo.edu/>.

FEATURES
source Location/Qualifiers
1..635

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="20"
/clone="692H20"

ORIGIN

Query Match 3.7%; Score 116; DB 10; Length 635;
Best Local Similarity 100.0%; Pred. No. 4.2e-54;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 947 AGGCTATATCAAGTACTGCACTCTTATGGCTACTACAACACGAGACATCG 1006
|||||
Db 520 AGGCTATATCAAGTACTGCACTCTTATGGCTACTACAACACGAGACATCG 579

QY 1007 GGTGGCTGAGGTACCGGCTGCTATGGCTTATGGTGGGGGTACGGTCTTC 1062
|||||
Db 580 GGTGGCTGAGGTACCGGCTGCTATGGCTTATGGTGGGGGTACGGTCTTC 635

Search completed: December 6, 2005, 03:55:58
Job time : 15660 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 30, 2005, 09:34:11 ; Search time 1705 Seconds
(without alignments)
12387.338 Million cell updates/sec

Title: US-10-792-307-3
Perfect score: 3169
Sequence: 1 gcagcgctcgcgcacatgag.....attcccaatccagaggaag 3169

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 110

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :
1: geneseqn21:.*
2: geneseqn1980s:.*
3: geneseqn1990s:.*
4: geneseqn2000s:.*
5: geneseqn2001as:.*
6: geneseqn2002as:.*
7: geneseqn2002bs:.*
8: geneseqn2003as:.*
9: geneseqn2003bs:.*
10: geneseqn2003cs:.*
11: geneseqn2003ds:.*
12: geneseqn2004as:.*
13: geneseqn2004bs:.*
14: geneseqn2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB ID | Description |
|------------|-------|-------|--------|-------------|--------------------|
| 1 | 3074 | 97.0 | 3121 | 8 ACC69614 | ACC69614 Human tfa |
| 2 | 1750 | 55.2 | 5027 | 5 AAS92296 | AAS92296 DNA encod |
| 3 | 493 | 15.6 | 2560 | 11 ADM01657 | ADM01657 Human cDN |
| 4 | 359 | 11.3 | 2591 | 6 ABV75613 | ABV75613 Human r1b |

ALIGNMENTS

RESULT 1

ACC69614

ID ACC69614 standard; cDNA; 3121 BP.

XX ACC69614;

XX ACC69614;

XX ACC69614;

XX ACC69614;

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XX ACC69614;

comprising a nucleic acid comprising the wild-type TDC1 or TDC2 gene

and/or mutant TDC1 or TDC2 gene obtained from the animal; (4) a method

for treating an animal prophylactically or therapeutically for hearing

loss due to a complete or partial loss of wild type TDC1 or TDC2; and (5)

a method for identifying one or more agents that interact with a TDC1

and/or TDC2 genes in a cell by administering one or more agents to the

cell comprising the genes and assaying the expression level of the genes

by the cell, where an increase or decrease in the expression level is

indicative of the interaction between the agents and the genes in the

cell. TDC1 and TDC2 have auditory activities and can be used in gene

therapy. The molecules, compositions and methods of the present invention

can be used for prognosticating, treating and monitoring hearing loss

XX Sequence 3121 BP; 778 A; 823 C; 824 G; 696 T; 0 U; 0 Other;

SQ

Query Match 97.0%; Score 3074; DB 8; Length 3121;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3074; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

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|----|------|---|------|
| Db | 588 | TGCTTACAAAGATGCTGATGGCCAGAAATGGGTCAAATTAAAGAGACTTTGATTAATT | 647 |
| QY | 696 | CAAGACTCATGTATCCCCGGGAAATGAAAGATCAAGACATTGAAAGTCACTTTGGTTC | 755 |
| Db | 648 | CAAGACTCATGTATCCCCGGGAAATGAAAGATCAAGACATTGAAAGTCACTTTGGTTC | 707 |
| QY | 756 | TTCAGTGGCATCGTATTTTCACTTTCTCCGATGGATGTATGGAGTTAACTTGTCTTTT | 815 |
| Db | 708 | TTCAGTGGCATCGTATTTTCACTTTCTCCGATGGATGTATGGAGTTAACTTGTCTTTT | 767 |
| QY | 816 | TGGCTTAATATTTGGTCTAGTCATTAATCCAGAGTAAGTGAATGGGCATGGCCCTATGGAG | 875 |
| Db | 768 | TGGCTTAATATTTGGTCTAGTCATTAATCCAGAGTAAGTGAATGGGCATGGCCCTATGGAG | 827 |
| QY | 876 | TATTCAGAAAAGACGTGCCCTGGGGCTGAAGAAAGAAAGGCCATGGATTTTCTGTCT | 935 |
| Db | 828 | TATTCAGAAAAGACGTGCCCTGGGGCTGAAGAAAGAAAGGCCATGGATTTTCTGTCT | 887 |
| QY | 936 | TTGGGATTTGAGGGCTATATCAAGTAAGTCTGCACTCTTCTATGGCTACTACAAACA | 995 |
| Db | 888 | TTGGGATTTGAGGGCTATATCAAGTAAGTCTGCACTCTTCTATGGCTACTACAAACA | 947 |
| QY | 996 | GAGCAACATCGGGTGGCTGAGGTACGGGGTGGCTATGGCTTACTTTATGGTGGGGTCA | 1055 |
| Db | 948 | GAGCAACATCGGGTGGCTGAGGTACGGGGTGGCTATGGCTTACTTTATGGTGGGGTCA | 1007 |
| QY | 1056 | CGTGTTCGGCTACAGCCTGATTTATTTGTCAATTCGATCGATGGCCACGCAATACCCAGAG | 1115 |
| Db | 1008 | CGTGTTCGGCTACAGCCTGATTTATTTGTCAATTCGATGGCCACGCAATACCCAGAG | 1067 |
| QY | 1116 | CAAGGCGAAGGGGAGAGTGAACAATTCACTTCAAGCTTCAAGATGTTCAACAGCTGGGA | 1175 |
| Db | 1068 | CAAGGCGAAGGGGAGAGTGAACAATTCACTTCAAGCTTCAAGATGTTCAACAGCTGGGA | 1127 |
| QY | 1176 | CTACCTGATCGGGAAATTCAGACAGCTGATTAACAAATATGCATCCATCAACCAAGCTT | 1235 |
| Db | 1128 | CTACCTGATCGGGAAATTCAGACAGCTGATTAACAAATATGCATCCATCAACCAAGCTT | 1187 |
| QY | 1236 | CAAGGAATCAATAGTGAATGAAACAAGAGTAAGCAAGAAATATCCATCTGACAG | 1295 |
| Db | 1188 | CAAGGAATCAATAGTGAATGAAACAAGAGTAAGCAAGAAATATCCATCTGACAG | 1247 |
| QY | 1296 | ATTTCTTGTGTCTGTGGCACTTTCTCATCATCTGCTGTTGTGTGAAGTGGGTACCT | 1355 |
| Db | 1248 | ATTTCTTGTGTCTGTGGCACTTTCTCATCATCTGCTGTTGTGTGAAGTGGGTACCT | 1307 |
| QY | 1356 | CATTACTTTGTGTTAAGCGATCTCAGCAATCTCCAAATGCAGAAATGTCAAGCTGGTA | 1415 |
| Db | 1308 | CATTACTTTGTGTTAAGCGATCTCAGCAATCTCCAAATGCAGAAATGTCAAGCTGGTA | 1367 |
| QY | 1416 | TGAAAGGAATGAGGTAGAGATCGTATGTCCCTGCTTGAATGTTTTGTCCCTCTGTT | 1475 |
| Db | 1368 | TGAAAGGAATGAGGTAGAGATCGTATGTCCCTGCTTGAATGTTTTGTCCCTCTGTT | 1427 |
| QY | 1476 | TGAAACATGCGCTGCCCTGGAGAAATTAACAACCAAGCATGGAAGTGAAGGAGCTGG | 1535 |
| Db | 1428 | TGAAACATGCGCTGCCCTGGAGAAATTAACAACCAAGCATGGAAGTGAAGGAGCTGG | 1487 |
| QY | 1536 | ACGCATCTTTGCACTCTTCTCTGGGGACCTCTACACATTTTCTCTGGCCCTGATGATGA | 1595 |
| Db | 1488 | ACGCATCTTTGCACTCTTCTCTGGGGACCTCTACACATTTTCTCTGGCCCTGATGATGA | 1547 |
| QY | 1596 | CGTCAACCTCAAGCTTGGCTAATGAAGACATTAAGAACTCACTGAGACTCTGTT | 1655 |
| Db | 1548 | CGTCAACCTCAAGCTTGGCTAATGAAGACATTAAGAACTCACTGAGACTCTGTT | 1607 |
| QY | 1656 | TAACTATTACACTCTCTGGTTGGAAAGAGTGTCCCGGACCAACCCCTGACCCCTGC | 1715 |
| Db | 1608 | TAACTATTACACTCTCTGGTTGGAAAGAGTGTCCCGGACCAACCCCTGACCCCTGC | 1667 |
| QY | 1716 | AGATGTGCCCGGGGTTCTTGGTGGAGAGACGTGTGGGCAATTGAATTCATGAGGCTGAC | 1775 |
| Db | 1668 | AGATGTGCCCGGGGTTCTTGGTGGAGAGACGTGTGGGCAATTGAATTCATGAGGCTGAC | 1727 |
| QY | 1776 | GGTGTGACATGCTGGTAAAGTACATCAATCCCTGCTGGGGGAACTTCTTAACGGCTTG | 1835 |
| Db | 1728 | GGTGTGACATGCTGGTAAAGTACATCAATCCCTGCTGGGGGAACTTCTTAACGGCTTG | 1787 |
| QY | 1836 | TTTTGTGGGTTCAATGAACACTACTGCTGGTGGTGGGACTTTGGAGGCTGAATTTCTTAT | 1895 |
| Db | 1788 | TTTTGTGGGTTCAATGAACACTACTGCTGGTGGTGGGACTTTGGAGGCTGAATTTCTTAT | 1847 |
| QY | 1896 | TGCTGAGTTTGATTAAGTGAATGTGCTGGGTTTGATCTTCAACAAAGAAATGATCTG | 1955 |
| Db | 1848 | TGCTGAGTTTGATTAAGTGAATGTGCTGGGTTTGATCTTCAACAAAGAAATGATCTG | 1907 |
| QY | 1956 | GATGGGCTCCTTCTATGCTCAAGGCTGTGGGCAATTAATGTGTGCGGCTGCTGAAGCTC | 2015 |
| Db | 1908 | GATGGGCTCCTTCTATGCTCAAGGCTGTGGGCAATTAATGTGTGCGGCTGCTGAAGCTC | 1967 |
| QY | 2016 | CATGACTTCCAGTCTGGGGGGTGAATGAGACAAAGTAAACCCATGAACGCGTTTCAA | 2075 |
| Db | 1968 | CATGACTTCCAGTCTGGGGGGTGAATGAGACAAAGTAAACCCATGAACGCGTTTCAA | 2027 |
| QY | 2076 | AGCCTCCGATCCAAACAATTCTACATGGGCTCCTGCTGGTGGTCTCTCAAGCCT | 2135 |
| Db | 2028 | AGCCTCCGATCCAAACAATTCTACATGGGCTCCTGCTGGTGGTCTCTCAAGCCT | 2087 |
| QY | 2136 | CCTGGCGTGGGCTACACATCATGTGCTCCACCCCTCCTTGAGCTGTGGGCGGTTCA | 2195 |
| Db | 2088 | CCTGGCGTGGGCTACACATCATGTGCTCCACCCCTCCTTGAGCTGTGGGCGGTTCA | 2147 |
| QY | 2196 | TGGGAAAACAGATGTACGATGTCTTCCAAAGACAAATTGAAGATTTCCCAACTT | 2255 |
| Db | 2148 | TGGGAAAACAGATGTACGATGTCTTCCAAAGACAAATTGAAGATTTCCCAACTT | 2207 |
| QY | 2256 | CCTGGGAGATCTTTGCTTTCTCTGCCAATCCAGGCTGATCAATCCAGCCATCCTGCT | 2315 |
| Db | 2208 | CCTGGGAGATCTTTGCTTTCTCTGCCAATCCAGGCTGATCAATCCAGCCATCCTGCT | 2267 |
| QY | 2316 | GATGTTCTTGGCATTTAAGTCACTGAGTCAAGTTTCCAAAAGCCTTTCCGAGTAATGC | 2375 |
| Db | 2268 | GATGTTCTTGGCATTTAAGTCACTGAGTCAAGTTTCCAAAAGCCTTTCCGAGTAATGC | 2327 |

QY 2376 CCAAGCTGAGGAGAAAAATCCAAAGTCTCCGTGAAGTTGAGAAAGTCACAAAATCTGTAAA 2435
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2328 CCAAGCTGAGGAGAAAAATCCAAAGTCTCCGTGAAGTTGAGAAAGTCACAAAATCTGTAAA 2487
 QY 2436 AGGCAAAAGCCACGCCAGATTCAGAGGACACACCTAAAACAGCTCCAAAATGCGAC 2495
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2388 AGGCAAAAGCCACGCCAGATTCAGAGGACACACCTAAAACAGCTCCAAAATGCGAC 2447
 QY 2496 CCAAGCTCCAACTCACAAGGAAAGACACTCTCCCTGCTGCCAGCCAAAGCCAGGCGAT 2555
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 Db 2508 GAGCAAGAAAGGCGCAGAGGCGCTGGGAAGCTCCAAATTCCTCCAGACAGACACTGCTGC 2567
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 Db 2568 CTCTGACACCTTCCATATCTGAGGCGCGCTGGAAATCGGACCAAGTTCTGGCAGGCGCC 2627
 QY 2676 ATCTCAGACTCATCCGTGAAGTCAAGCTCTGAAAGAGTGGTGAAGACACTCCCACTG 2735
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 Db 2628 ATCTCAGACTCATCCGTGAAGTCAAGCTCTGAAAGAGTGGTGAAGACACTCCCACTG 2687
 QY 2736 ACGGCTAGGACTCAGAGGAGCTGACCTAGGGCTGATCTCAAATACCCCAATTTTCA 2795
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 Db 2688 ACGGCTAGGACTCAGAGGAGCTGACCTAGGGCTGATCTCAAATACCCCAATTTTCA 2747
 QY 2796 AACTACCAAAACAAGGTTCTCTCCCTCTTCTCTCTCAATACATGCTGCTCTCTC 2855
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 Db 2748 AACTACCAAAACAAGGTTCTCTCCCTCTTCTCTCTCAATACATGCTGCTCTCTCTC 2807
 QY 2856 TTGGAATGATGAATTTGATTCCTTCAAGGCGCTTGTCAAGTACCGAAGGAGAAAGACG 2915
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 Db 2808 TTGGAATGATGAATTTGATTCCTTCAAGGCGCTTGTCAAGTACCGAAGGAGAAAGACG 2867
 QY 2916 TGGCTTCACTGCTCTTAAAGGAAGTGGAGCATCTGTCACTAACTGCCCTCCCAAT 2975
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2868 TGGCTTCACTGCTCTTAAAGGAAGTGGAGCATCTGTCACTAACTGCCCTCCCAAT 2927
 QY 2976 ATCTTGGTTCAAGAGCTCTGAACCCCAAGCTCAAGTGGTGAAGCTTGGCTCCGATTT 3035
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2928 ATCTTGGTTCAAGAGCTCTGAACCCCAAGCTCAAGTGGTGAAGCTTGGCTCCGATTT 2987
 QY 3036 TCGAGTTGGGAAAGGCGCATGACACCTCGTAGACTTTTCCATGGGATACAGTTTAA 3095
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2988 TCGAGTTGGGAAAGGCGCATGACACCTCGTAGACTTTTCCATGGGATACAGTTTAA 3047
 QY 3096 GACAGGGGTTTCTGCCAGCTTCCCTAAACAAGAGGGGATGGAAGAGGCGCTACATTTCT 3155
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3048 GACAGGGGTTTCTGCCAGCTTCCCTAAACAAGAGGGGATGGAAGAGGCGCTACATTTCT 3107
 QY 3156 CAATCCAGAGGAAG 3169
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 Db 3108 CAATCCAGAGGAAG 3121

RESULT 2
 ID AAS92296
 XX AAS92296 standard; cDNA; 5027 BP.
 AC AAS92296;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #28100.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 PN W0200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HSE-) HSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639462/73.
 DR P-PSDB; A8628109.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 1; SEQ ID NO 28100; 103bp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping.
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS94197-AAS94364 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in

| | | | |
|----|------|---|------|
| QY | 166 | ACTCTTCGGTTGGAGAGAGATGTCCCCAGCAACCCCTGCACCTCGAGATGTGGCC | 1726 |
| Db | 1814 | ACTCTTCGGTTGGAGAGAGAGATGTCCCCAGCAACCCCTGCACCTCGAGATGTGGCC | 1873 |
| QY | 1727 | GGGGTCTTCCTCGTGGAGACAGCTGTGGGCAATTGAATTACAGAGCTGACCGTGTGACA | 1786 |
| Db | 1874 | GGGGTCTTCCTCGTGGAGAGACAGCTGTGGGCAATTGAATTACAGAGCTGACCGTGTGACA | 1933 |
| QY | 1787 | TGCTGTTAAAGTACATGACATTCCTGCTGGGGGACTTCCTAGCGGGCTGTTTTGTGGGT | 1846 |
| Db | 1934 | TGCTGTTAAAGTACATGACATTCCTGCTGGGGGACTTCCTAGCGGGCTGTTTTGTGGGT | 1993 |
| QY | 1847 | TGATGAACACTGCTGGTGGTGGGACTTGGAGGCTGGATTTCTTCATATGCTGAGTTTG | 1906 |
| Db | 1994 | TGATGAACACTGCTGGTGGTGGGACTTGGAGGCTGGATTTCTTCATATGCTGAGTTTG | 2053 |
| QY | 1907 | ATATTAGTGAAGATGTGCTGGGTTTATCTTCACACAGAGATGATGAGTGGGCTCT | 1966 |
| Db | 2054 | ATATTAGTGAAGATGTGCTGGGTTTATCTTCACACAGAGATGATGAGTGGGCTCT | 2113 |
| QY | 1967 | TGTAATGCTCGAGGCTGGTGGGCAATTATGTGCTGGGCTGCTGACCTGCATGTACTTC | 2026 |
| Db | 2114 | TGTAATGCTCGAGGCTGGTGGGCAATTATGTGCTGGGCTGCTGACCTGCATGTACTTC | 2173 |
| QY | 2027 | ATGTGCTGGAGGGTGTATGACGACAACTGACCCATGAGCGCTGTTCAAGGCTCCCGAT | 2086 |
| Db | 2174 | ATGTGCTGGAGGGTGTATGACGACAACTGACCCATGAGCGCTGTTCAAGGCTCCCGAT | 2233 |
| QY | 2087 | CCAGAACCTTCATCATGGGCTCCTGCTGCTGTGGTCTTCTTCAGGCTCCTGCCGGTGG | 2146 |
| Db | 2234 | CCAGAACCTTCATCATGGGCTCCTGCTGCTGTGGTCTTCTTCAGGCTCCTGCCGGTGG | 2293 |
| QY | 2147 | CCGACACATCATGTCCCTCCACACCTCCTTGACTGCGGGCCGTTGAGTGGGAAAAACA | 2206 |
| Db | 2294 | CCGACACATCATGTCCCTCCACACCTCCTTGACTGCGGGCCGTTGAGTGGGAAAAACA | 2353 |
| QY | 2207 | GAAATGTACGATGCTCCTCCAGAGACAACTTGAAACAGATTTCCACACTTCTGGGCAAGA | 2266 |
| Db | 2354 | GAAATGTACGATGCTCCTCCAGAGACAACTTGAAACAGATTTCCACACTTCTGGGCAAGA | 2413 |
| QY | 2267 | TGTTTTGCTTCCTGGCCATCCAGGCGCTGATCATCCAGCAGCTGCTGCTGATGTTCTTGG | 2326 |
| Db | 2414 | TGTTTTGCTTCCTGGCCATCCAGGCGCTGATCATCCAGCAGCTGCTGCTGATGTTCTTGG | 2473 |
| QY | 2327 | CCATTTACTACCTGAACCTCAGTTTCCAAAAGGCTTTCGAGAGCTAATGCCACGCTGAGGA | 2386 |
| Db | 2474 | CCATTTACTACCTGAACCTCAGTTTCCAAAAGGCTTTCGAGAGCTAATGCCACGCTGAGGA | 2533 |
| QY | 2387 | AGAAATCCAGATGCTCCGTGAAGTTGAGAGAGTCACAAACTGTGAAAAGCAAAAGCA | 2446 |
| Db | 2534 | AGAAATCCAGATGCTCCGTGAAGTTGAGAGAGTCACAAACTGTGAAAAGCAAAAGCA | 2593 |
| QY | 2447 | CAGCGAGATTCAGAGAGACACCTTAAAGGAGCTGCCAAAATGCCACCGCAGCTCCAGC | 2506 |
| Db | 2594 | CAGCGAGATTCAGAGAGACACCTTAAAGGAGCTGCCAAAATGCCACCGCAGCTCCAGC | 2653 |
| QY | 2507 | TGACCAAGAGAGACACTCCTCCCTCTGCCAGCCAAAGCCAGGCAATGACACAGAGAG | 2566 |

|||||
Db 2654 TCACCAAGAGAGACCACTCCTCCTGCGAGCCAAAGCCAGCCATGACAAAGAG 2713
QY 2567 CCGAGGGCCCTGGAGCTCCATTTGCGACAGAGACACACTGCTGCTGTGAGACCC 2626
|||||
Db 2714 CCGAGGGCCCTGGAGCTCCATTTGCGACAGAGACACACTGCTGCTGTGAGACCC 2773
QY 2627 TTCTATATCTCGGCCCTGGAATCGAGACAGATTCTGGCCAGCCCATCTGAGACTC 2686
|||||
Db 2774 TTCTATATCTCGGCCCTGGAATCGAGACAGATTCTGGCCAGCCCATCTGAGACTC 2833
QY 2687 ATCCGTGGAG 2696
|||||
Db 2834 ATCCGTGGAG 2843

RESULT 3
ADM01657
ID ADM01657 standard; cDNA; 2560 BP.
XX
AC ADM01657;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human cDNA of the invention SEQ ID NO:342.
XX
KW 5s3 gene; human; gene therapy; diagnostic marker; pharmaceutical.
XX
OS Homo sapiens.
XX
PN EPI347046-A1.
XX
PD 24-SEP-2003.
XX
PF 12-APR-2002; 2002EP-00008400.
XX
PR 22-MAR-2002; 2002JP-00137785.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isegai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,
PI Yamamoto J, Isono Y, Hiro Y, Otsuka K, Negai K, Irie R, Tamechika I,
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y.
XX
DR WPI; 2003-723558/69.
DR P-PSDB; ADM04100.
XX
PT New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX
PS Claim 1; SEQ ID NO 342; 3055p; English.
CC The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for

CC detecting the polynucleotide. The polynucleotides ADM0316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC cDNA sequence of the invention.
XX
SQ Sequence 2560 BP; 568 A; 652 C; 568 G; 772 T; 0 U; 0 Other;
Query Match 15.6%; Score 493; DB 11; Length 2560;
Best Local Similarity 99.7%; Pred. No. 3,2e-226;
Matches 593; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1293 AAGATTTCTTCGTGCTGCGCAACTTTCTCATCATCTGCTTTGTGTGAGAGTGGGTA 1352
|||||
Db 1 AAGATTTCTTCGTGCTGCGCAACTTTCTCATCATCTGCTTTGTGTGAGAGTGGGTA 60
|||||
QY 1353 CCTCATTTACTTTGGGTTAAGGATCGACGAAATTCGAAATTCGAAATTCGAGCTG 1412
|||||
Db 61 CCTCATTTACTTTGGGTTAAGGATCGACGAAATTTCCAAATTCGAAATTCGAGCTG 120
|||||
QY 1413 GTATGAAAGGATGAGGTAGAGATCGATGTCCTGCTTGAATGTTTTGTCCCCCTCT 1472
|||||
Db 121 GTATGAAAGGATGAGGTAGAGATCGATGTCCTGCTTGAATGTTTTGTCCCCCTCT 180
|||||
QY 1473 GTTTGAAACCATCGCTGCGCTGGAAGATTACACCCAGCAGCTGAGTGAAGTGGACCT 1532
|||||
Db 181 GTTTGAAACCATCGCTGCGCTGGAAGATTACACCCAGCAGCTGAGTGAAGTGGACCT 240
|||||
QY 1533 GGAAGCATCTTTGCACTCTCCTGAGGAACTCTACACATTTCTCTGAGCCCTGANTGA 1592
|||||
Db 241 GGAAGCATCTTTGCACTCTCCTGAGGAACTCTACACATTTCTCTGAGCCCTGANTGA 300
|||||
QY 1593 TGAAGTCACCTCAAGCTTGTCTAATGAAGACATAAAGAACATCACTCACTGACTCT 1652
|||||
Db 301 TGAAGTCACCTCAAGCTTGTCTAATGAAGACATAAAGAACATCACTCACTGACTCT 360
|||||
QY 1653 GTTTAACTATTACAACTCTTGTGTGGAACGAGAGTGTCCCCGACACACCCCTGCAACC 1712
|||||
Db 361 GTTTAACTATTACAACTCTTGTGTGGAACGAGAGTGTCCCCGACACACCCCTGCAACC 420
|||||
QY 1713 TCAGATGTGCCCCGAGGTTCTTGCTGGAGACAGCTGTGGGCAATTGAATTCATGAGCT 1772
|||||
Db 421 TCAGATGTGCCCCGAGGTTCTTGCTGGAGACAGCTGTGGGCAATTGAATTCATGAGCT 480
|||||
QY 1773 GAGGTTGTGACATGCTGGTAACGTACATCACTCTGCTGAGGGAAGTTCTACGGGC 1832
|||||
Db 481 GAGGTTGTGACATGCTGGTAACGTACATCACTCTGCTGAGGGAAGTTCTACGGGC 540
|||||
QY 1833 TTGTTTGTGCGGTTTCATGAACACTGCTGTGCTGGACCTTGGAGGCTGGATT 1887
|||||
Db 541 TTGTTTGTGCGGTTTCATGAACACTGCTGTGCTGGAGCTTGGAGGCTGGATT 595
|||||

RESULT 4
ABV75613
ID ABV75613 standard; cDNA; 2591 BP.

XX ABV75613;
AC 23-JAN-2003 (first entry)
XX
DT Human ribosomal protein L3220.9 cDNA.
XX
DE Human ribosomal protein L3220.9 cDNA.
XX
KW Human; ribosomal protein L3220.9; diabetes; menstrual disorder; anaemia;
KW peptic ulcer; arrhythmia; epilepsy; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 74..646
FT /*tag= a
FT /product= "Ribosomal protein L3220.9"
XX
PN CNI345827-A.
XX
PD 24-APR-2002.
XX
PF 29-SEP-2000; 2000CN-00125511.
XX
PR 29-SEP-2000; 2000CN-00125511.
XX
PA (SHAN-) SHANGHAI BOWINDOW GENE DEV INC.
XX
PI Mao Y., Xie Y;
XX
DR WPI; 2002-548952/59.
DR P-PSDB; ABP57746.
XX
PT Novel polypeptide-human ribosomal protein L3220.9 and encoding
PT polynucleotide for treating diabetes, menstrual disorder, peptic ulcer,
PT arrhythmia, anemia and epilepsy.
XX
PS Claim 6; Page 25-26 (Disclosure); 33pp; Chinese.
XX
CC The invention relates to the novel human ribosomal protein L3220.9, and
CC the polynucleotide encoding it. The protein is useful for treating
CC diabetes, menstrual disorder, peptic ulcer, arrhythmia, anaemia and
CC epilepsy. Also disclosed is an antagonist for resisting the polypeptide
CC and its therapeutic action, and the application of the polynucleotide.
CC The present sequence encodes the human ribosomal protein L3220.9 of the
CC invention
XX
SQ Sequence 2591 BP; 576 A; 670 C; 557 G; 788 T; 0 U; 0 Other;
XX
Query Match 11.3%; Score 359; DB 6; Length 2591;
Best Local Similarity 99.6%; Pred. No. 9.9e-162;
Matches 459; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1427 AGGTAGAGATCGATGCGCTGCTGGATGTTTGTCCCTCTGTTGAACATCG 1486
DB 60 AGGTAGAGATCGATGCGCTGCTGGATGTTTGTCCCTCTGTTGAACATCG 119
QY 1487 CTGCCCTGGAGATTACCAACCAAGCACTGAGTGAAGTGACAGTGGACCACTTTG 1546

DB 120 CTGCCCTGGAGATTACCAACCAAGCACTGAGTGAAGTGACAGTGGACCACTTTG 179
QY 1547 CACTCTTCCTGGAGAACCTCTACATTTCTTGGCCCTGATGATGACGTCACCTCA 1606
DB 180 CACTCTTCCTGGAGAACCTCTACATTTCTTGGCCCTGATGATGATGTCACCTCA 239
QY 1607 AGCTTGCTAATGAGAGACATTAAGAAATCAGTCACTGAGCTGTTTAACTATTACA 1666
DB 240 AGCTTGCTAATGAGAGACATTAAGAAATCAGTCACTGAGCTGTTTAACTATTACA 299
QY 1667 ACTCTTCCTGGTGAAGAGAGTGTCCCGACCAACCCCTGCACCCCTGCAATGTGCCCC 1726
DB 300 ACTCTTCCTGGTGAAGAGAGTGTCCCGACCAACCCCTGCACCCCTGCAATGTGCCCC 359
QY 1727 GGGGTTCTGCTGGAGACAGCTGTGGGCAATTGAATCATGAGCTGACGGTGTGACA 1786
DB 360 GGGGTTCTGCTGGAGACAGCTGTGGGCAATTGAATCATGAGCTGACGGTGTGACA 419
QY 1787 TCTGTGTAACGTACATGACCATCTGCTGGGGACTTCTACGGGCTGTGTTGTGGCT 1846
DB 420 TCTGTGTAACGTACATGACCATCTGCTGGGGACTTCTACGGGCTGTGTTGTGGCT 479
QY 1847 TCATGAACTAAGTGTGCTGGGACTTGGAGCTTGGATTT 1887
DB 480 TCATGAACTAAGTGTGCTGGGACTTGGAGCTTGGATTT 520
RESULT 5
ADR07551
ID ADR07551 standard; cDNA, 3566 BP.
AC ADR07551;
XX
DT 04-NOV-2004 (first entry)
XX
DE Full length human cDNA useful for treating neurological disease Seq 1057.
XX
DE gene; ss; human; oligo-capping method; diagnostic marker; gene therapy;
KW osteoporosis; neurological disease; Alzheimer's disease;
KW Parkinson's disease; dementia; short memory; cancer;
KW sense or motor function; emotional reaction; fear response; panic;
KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
KW tranquilizer.
XX
OS Homo sapiens.
XX
PN EPI447413-A2.
XX
PD 18-AUG-2004.
XX
PF 12-FEB-2004; 2004EP-00003145.
XX
PR 14-FEB-2003; 2003JP-00102207.
PR 09-MAY-2003; 2003JP-00131452.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Yamamoto J, Nishikawa T, Iseno Y, Sugiyama T, Otsuki T;
PI Wakematsu A, Ishii S, Nagai K, Irie R;
XX
DR WPI: 2004-583265/57.
DR P-P9DB; ADR09507.
XX
PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS Claim 1; SEQ ID NO 1057; 2686bp; English.
XX
CC This invention relates to novel, isolated full length human cDNA
CC molecules and the encoded proteins thereof. Specifically, it refers to
CC cDNA clones obtained by an oligo-capping method, where none of these
CC clones are identical to any known human mRNAs. The present invention
CC describes an immunassay to identify agonists and antagonists, as well as
CC antibodies, antisense molecules and siRNAs that can all be used to bind
CC to and modulate expression of the cDNA molecules. As such, these
CC molecules are useful for diagnostic markers or therapeutic targets for
CC the various diseases or morbid states. In particular, they are useful in
CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's
CC disease, Parkinson's disease, dementia, short memory and various cancers,
CC as well as for maintaining equilibrium of sense or motor function, and
CC for treating emotional reaction, fear response and panic. Accordingly,
CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
CC cyostatic and tranquilliser activities. This polynucleotide is a full
CC length human cDNA sequence of the invention. NOTE: This sequence is not
CC given in the sequence listing of the specification but can be obtained on
CC CD-ROM from the European Patent Office, Vienna Sub-office.
XX
SQ Sequence 3566 Bp; 989 A; 791 C; 877 G; 909 T; 0 U; 0 Other;

Query Match 9.7%; Score 308; DB 13; Length 3566;
Best Local Similarity 100.0%; Pred. No. 3.5e-137;
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1888 CCTCATATGCTGAGTTGATATTAGTGAATGCTGGTTGATCTTCAACCAAGA 1947
DB 163 CCTCATATGCTGAGTTGATATTAGTGAATGCTGGTTGATCTTCAACCAAGA 222
QY 1948 ATGATCTGATGGGCTCCTTATAGCTCCAGGCTGGTGGGATTAATGTCGTGGGCTG 2007
DB 223 ATGATCTGATGGGCTCCTTATAGCTCCAGGCTGGTGGGATTAATGTCGTGGGCTG 282
QY 2008 CTGACCTTCATGACTTCAAGTCTGGGCGGTGATGAGCAAGAACTACCCATGAACG 2067
DB 283 CTGACCTTCATGACTTCAAGTCTGGGCGGTGATGAGCAAGAACTACCCATGAACG 342
QY 2068 GTGTTCAAAGCTCCCGATCCAAACAATTCTACATGGGCTCTGCTGCTGGTGGCTTTC 2127
DB 343 GTGTTCAAAGCTCCCGATCCAAACAATTCTACATGGGCTCTGCTGCTGGTGGCTTTC 402
QY 2128 CTGAGGCTCCTGGGCGGTGCTCAACAATGATGCTCCCAAGCTCTTGACTGGGCG 2187
DB 403 CTGAGGCTCCTGGGCGGTGCTCAACAATGATGCTCCCAAGCTCTTGACTGGGCG 462

QY 2188 CCGTTCAG 2195
DB 463 CCGTTCAG 470
Search completed: November 30, 2005, 14:00:45
Job time : 1707 secs

OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 12:30:01 ; Search time 541 Seconds
(without alignments)
10412.371 Million cell updates/sec

Title: US-10-792-307-3
Perfect score: 3169
Sequence: 1 gcagtcgtctgcacacagag.....attccatccacagagag 3169

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 110

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- Issued Patents_NA:*
- 1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
 - 2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
 - 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
 - 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
 - 5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
 - 6: /cgn2_6/ptodata/1/ina/PGTUS_COMB.seq:*
 - 7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
 - 8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
 - 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Match | Score | Length | DB ID | Description |
|------------------|-------------|-------|--------|-------|-------------|
| No matches found | | | | | |

Search completed: December 5, 2005, 20:14:30
Job time : 541 secs

OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 12:30:09 ; Search time 2435 Seconds
(without alignments)
10762.076 Million cell updates/sec

Title: US-10-792-307-3
Perfect score: 3169
Sequence: 1 gcagtcgtctgcacacagag.....attccatccacagagag 3169

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 110

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- Published Applications_NA_Main:*
- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
 - 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
 - 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
 - 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
 - 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
 - 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
 - 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
 - 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
 - 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
 - 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Match | Score | Length | DB ID | Description |
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| 2 | 3074 | 97.0 | 3121 | 8 | US-10-487-887-3 |
| 3 | 1750 | 55.2 | 5027 | 9 | US-10-450-763-28100 |
| 4 | 1648 | 52.0 | 4895 | 6 | US-10-115-831-134 |
| 5 | 493 | 15.6 | 2860 | 6 | US-10-108-260A-342 |
| 6 | 153 | 4.8 | 1060 | 5 | US-10-027-632-122322 |
| 7 | 153 | 4.8 | 1060 | 6 | US-10-027-632-122322 |

ALIGNMENTS

```
RESULT 1
US-10-792-307-3
; Sequence 3, Application US/10792307
; Publication No. US20050196759A1
; GENERAL INFORMATION:
; APPLICANT: Grifith, Andrew J.
; APPLICANT: Kurilme, Kiyoto
; APPLICANT: Wilcox, Edward
; APPLICANT: Fiedeman, Thomas
; TITLE OF INVENTION: TRANSDUCTIN-1 AND TRANSDUCTIN-2 AND APPLICATIONS TO
HEREDITARY
; TITLE OF INVENTION: DEAFNESS
; FILE REFERENCE: 227540
; CURRENT APPLICATION NUMBER: US/10792,307
; CURRENT FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 3169
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-792-307-3

Query Match          100.0%; Score 3169; DB 9; Length 3169;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGTGTCTGTCAGCATGAGCCACAGTAAAGG3CCTGAAGAGAGAGCAGAGCGGA 60
Db 1 GCAGTGTCTGTCAGCATGAGCCACAGTAAAGG3CCTGAAGAGAGAGCAGAGCGGA 60

QY 61 GTGAAGGCGCGGTGAAGAGCGGCTCTCCACACACAGTGAACAGCTGGAGAGGATCC 120
Db 61 GTGAAGGCGCGGTGAAGAGCGGCTCTCCACACACAGTGAACAGCTGGAGAGGATCC 120

QY 121 TCAGCAAGCGGCTCTCAAGAGGAGGAGCCCAAGGAGGAGGAGGAGGAGGAGGAGG 180
Db 121 TCAGCAAGCGGCTCTCAAGAGGAGGAGCCCAAGGAGGAGGAGGAGGAGGAGGAGG 180

QY 181 CAGAGAGAGCGCGCGCGGAGAGCCCAAGCGGAGTCTCCCGAGAGAGAGAGGAGG 240
Db 181 CAGAGAGAGCGCGCGCGGAGAGCCCAAGCGGAGTCTCCCGAGAGAGAGAGGAGG 240

QY 241 CGCAGGAGACAGAGAGAGCTGGGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 300
Db 241 CGCAGGAGACAGAGAGAGCTGGGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 300

QY 301 GAGGCGAGAGAGAGGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
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QY 361 AGGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
Db 361 AGGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
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QY 1261 GAGAGTAAAGAAAGAAAAATATCATCTGACAGATTTCTTGGTGTCTGGCCAACTTT 1320
|||||
Db 1261 GAGAGTAAAGAAAGAAAAATATCATCTGACAGATTTCTTGGTGTCTGGCCAACTTT 1320
QY 1321 CTGATCATCTGCTGTTGTGTGTGGAAGTGGGTACCTCAATTTACTTTGTGGTTAAGCAATCT 1380
|||||
Db 1321 CTGATCATCTGCTGTTGTGTGTGGAAGTGGGTACCTCAATTTACTTTGTGGTTAAGCAATCT 1380
QY 1381 CAGCAATTCCTCAAAAATGCAATGCTGATGTGAATGAAGAAATGAGATGAGATGGTG 1440
|||||
Db 1381 CAGCAATTCCTCAAAAATGCAATGCTGATGTGAATGAAGAAATGAGATGAGATGGTG 1440
QY 1441 ATGTCCCTGCTTGGAAATGTTTGTCCCTCTGTTTGAAACCATGGTGGCCCTGGAGAAAT 1500
|||||
Db 1441 ATGTCCCTGCTTGGAAATGTTTGTCCCTCTGTTTGAAACCATGGTGGCCCTGGAGAAAT 1500
QY 1501 TACACCCACGCACTGGAAGTGAAGTGGAGCTGGAGACGATCTTTGCACTCTTCTGGGG 1560
|||||
Db 1501 TACACCCACGCACTGGAAGTGAAGTGGAGCTGGAGACGATCTTTGCACTCTTCTGGGG 1560
QY 1561 AACCTCTACACATTTCTGTTGGCCCTGATGATGATGATGATGATGATGATGATGATGATGAT 1620
|||||
Db 1561 AACCTCTACACATTTCTGTTGGCCCTGATGATGATGATGATGATGATGATGATGATGATGAT 1620
QY 1621 GAGACATTAAGAAATCACTCACTGGAATCTGTTTAATATTACAATCTTCTGGTTGG 1680
|||||
Db 1621 GAGACATTAAGAAATCACTCACTGGAATCTGTTTAATATTACAATCTTCTGGTTGG 1680
QY 1681 AACGAGAGTGTCCCGGACACACCCCTGACACCTGACAGATGTGCCCGGGGTTCTTGGCTGG 1740
|||||
Db 1681 AACGAGAGTGTCCCGGACACACCCCTGACACCTGACAGATGTGCCCGGGGTTCTTGGCTGG 1740
QY 1741 GAGACAGCTGTGGGCAATTGAATTCATGAGGCTGACGGTGTGACATGCTGGTAAAGTAC 1800
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Db 1741 GAGACAGCTGTGGGCAATTGAATTCATGAGGCTGACGGTGTGACATGCTGGTAAAGTAC 1800
QY 1801 ATCAACCATCTGCTGGGGGACCTTCTACGGGCTTGTTTGTGGGGTTCAATGAATCACTGC 1860
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Db 1801 ATCAACCATCTGCTGGGGGACCTTCTACGGGCTTGTTTGTGGGGTTCAATGAATCACTGC 1860
QY 1861 TGGTGTGGGCACTTGAAGGCTGGAATTCCTTCATATGCTGAGTTTGAATTAATGAGAAAT 1920
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Db 1861 TGGTGTGGGCACTTGAAGGCTGGAATTCCTTCATATGCTGAGTTTGAATTAATGAGAAAT 1920
QY 1921 GTGCTGGGTTTGAATCTTCAACCAAGGAATGATCTGATGGGCTCCTTCTATGCTCAAGGC 1980
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Db 1921 GTGCTGGGTTTGAATCTTCAACCAAGGAATGATCTGATGGGCTCCTTCTATGCTCAAGGC 1980
QY 1981 CTGGTGGGCAATTAATGTGCTGGGCTGCTGACCTCAATGTACTTCAAGTGTGGGCGGTG 2040
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Db 1981 CTGGTGGGCAATTAATGTGCTGGGCTGCTGACCTCAATGTACTTCAAGTGTGGGCGGTG 2040
QY 2041 ATGAGCAGCAAGCTACCCCAATGAACCGGTGTTCAAAAGCCTCCCATTCACAACTCTTAC 2100
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Db 2041 ATGAGCAGCAAGCTACCCCAATGAACCGGTGTTCAAAAGCCTCCCATTCACAACTCTTAC 2100

QY 2101 ATGGGCTCCTGCTGCTGATGCTCTTCTCAGGCTCCTTGGCGGTGGCTACACCATCATG 2160
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Db 2101 ATGGGCTCCTGCTGCTGATGCTCTTCTCAGGCTCCTTGGCGGTGGCTACACCATCATG 2160
QY 2161 TCCCTCCCAACCTCCTTTGATGCTGGGGGCGCTCAATGGGAAAAACGAATGTACGATGTC 2220
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Db 2161 TCCCTCCCAACCTCCTTTGATGCTGGGGGCGCTCAATGGGAAAAACGAATGTACGATGTC 2220
QY 2221 CTCGAGAGCAATTAAGAAACGATTTCCCAACCTTCTGGGCAAGATCTTTGCTTCTC 2280
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Db 2221 CTCGAGAGCAATTAAGAAACGATTTCCCAACCTTCTGGGCAAGATCTTTGCTTCTC 2280
QY 2281 GCAATCCAGGCTGATCATCCAGCAATCCTGATGATGTTCTTGGCAATTTACTACTG 2340
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Db 2281 GCAATCCAGGCTGATCATCCAGCAATCCTGATGATGTTCTTGGCAATTTACTACTG 2340
QY 2341 AACCTGATTTCCAAAAGGCTTTCCGAGCTTAATCCCAAGCTGAGGAAAGAAATGCAAGTG 2400
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Db 2341 AACCTGATTTCCAAAAGGCTTTCCGAGCTTAATCCCAAGCTGAGGAAAGAAATGCAAGTG 2400
QY 2401 CTGGTGAATGAGAGAGTCAAAATCTGTAAAGCAAAAGCAGAGCAAGATTCA 2460
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Db 2401 CTGGTGAATGAGAGAGTCAAAATCTGTAAAGCAAAAGCAGAGCAAGATTCA 2460
QY 2461 GAGGACACACTTAAAGCAGCTCAAAAATGCCACCAAGCTCAACTCAACAAAGAAAG 2520
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Db 2461 GAGGACACACTTAAAGCAGCTCAAAAATGCCACCAAGCTCAACTCAACAAAGAAAG 2520
QY 2521 AACCTGCTCCCTCTGGCAGCCAAAGCAGGCAATGAGAAAGGAGGAGGAGGAGGAGGAGG 2580
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Db 2521 AACCTGCTCCCTCTGGCAGCCAAAGCAGGCAATGAGAAAGGAGGAGGAGGAGGAGGAGGAGG 2580
QY 2581 AACCTCAATTTGCCAGCAGAGCAACTGCTGCTCTGGAACCTTCTATATCTCGG 2640
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Db 2581 AACCTCAATTTGCCAGCAGAGCAACTGCTGCTCTGGAACCTTCTATATCTCGG 2640
QY 2641 CCCCCTGAATGGAGCAGATTCGTGGCAGCCCATCTCAGACTCATCCGTGGAGGTCA 2700
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Db 2641 CCCCCTGAATGGAGCAGATTCGTGGCAGCCCATCTCAGACTCATCCGTGGAGGTCA 2700
QY 2701 GGCCTGTGAAAAGTGTCAAGAGCTCCCACTGACGGGCTAAGGACTCCAGGAGGCTCG 2760
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Db 2701 GGCCTGTGAAAAGTGTCAAGAGCTCCCACTGACGGGCTAAGGACTCCAGGAGGCTCG 2760
QY 2761 ACCCTAGGAGCTGATCCTCAAGTACCCAGTTTCAACATACCAAAAGGTTCTCTCC 2820
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Db 2761 ACCCTAGGAGCTGATCCTCAAGTACCCAGTTTCAACATACCAAAAGGTTCTCTCC 2820
QY 2821 CTCTTTCTCTCAATACATGCTGTGCTCCTCTTGAATGATGAATGAACTTTGATTCCT 2880
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Db 2821 CTCTTTCTCTCAATACATGCTGTGCTCCTCTTGAATGATGAATGAACTTTGATTCCT 2880
QY 2881 TCAAGGCGTTTGCAGCTAACCAAGGAGGAGCAAGTGGCTTCACTGCTTTTGGGAA 2940
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Db 2881 TCAAGGCGTTTGCAGCTAACCAAGGAGGAGCAAGTGGCTTCACTGCTTTTGGGAA 2940
QY 2941 CTGAGGCAATCTGTCACTAACTGGCCTCCCAATATCTTGGTTCAAGACGCTGTGAGC 3000

Db 2941 CTTGAGCCATCTCTGACTAACTGCCCTCCCAATATCTTGGTTCAACAGCTCGAAC 3000
Qy 3001 CGACGCTCAGAGTGGTGGACCTTGGCTCCCGATTTTCGAGTTGGGGAGGGGCATAGCC 3060
Db 3001 CGACGCTCAGAGTGGTGGACCTTGGCTCCCGATTTTCGAGTTGGGGAGGGGCATAGCC 3060
Qy 3061 ACCCTCGTAGCTTTTCCATGGGATACAGTTTAGAGCAGGGGTTTCTGCCAGCTTCCT 3120
Db 3061 ACCCTCGTAGCTTTTCCATGGGATACAGTTTAGAGCAGGGGTTTCTGCCAGCTTCCT 3120
Qy 3121 AACCAAGAGGGGAGTAGAAGGGCTACATTTCTCAATCCAGAGAG 3169
Db 3121 AACCAAGAGGGGAGTAGAAGGGCTACATTTCTCAATCCAGAGAG 3169

RESULT 2
US-10-487-887-3
; Sequence 3, Application US/10487887
; Publication No. US20040249139A1
; GENERAL INFORMATION:
; APPLICANT: Griffith, Andrew J
; APPLICANT: Wilcox, Edward
; APPLICANT: Friedman, Thomas
; TITLE OF INVENTION: TRANSDUCTIN-1 AND TRANSDUCTIN-2 AND APPLICATIONS TO HEREDITARY
; TITLE OF INVENTION: DEAFNESS
; FILE REFERENCE: 226544
; CURRENT APPLICATION NUMBER: US/10/487,887
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/US02/29614
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/323,275
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent version 3.2
; SEQ ID NO 3
; LENGTH: 3121
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-487-887-3

Query Match 97.0%; Score 3074; DB 8; Length 3121;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3074; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 96 AGGTGACAGGCTGGAGGAAGATCTCAAGCAAGCGGCTCAAAAGCCGAGGGAGCC 155
Db 48 AGGTGACAGGCTGGAGGAAGATCTCAAGCAAGCGGCTCAAAAGCCGAGGGAGCC 107
Qy 156 AGGCAAGCGGAGGCTCAGCGAAGCCAGAGGAGCGGCGGGGCAAGCCAGCCGAG 215
Db 108 AGGCAAGCGGAGGCTCAGCGAAGCCAGAGGAGCGGCGGGGCAAGCCAGCCGAG 167
Qy 216 GTCTCCCGAGGAGCAAGAGGGCGCAGAGACAGAGAGAGCTGGGGAGCAAG 275

Db 168 GTCTCCCGAGGAGCAAGAGGGCGCAGAGACAGAGAGAGCTGGGGAGCAAG 227
Qy 276 GCGGGGAGGAGCAGAGAGGAGCTGCCAGGCGAGAGAAAGCGAGAGAGGCGCTCTT 335
Db 228 GCGGGGAGGAGCAGAGAGGAGCTGCCAGGCGAGAGAAAGCGAGAGGCGCTCTT 287
Qy 336 CCAAGAGCGAGCAGAGCGCCAAAGAGGAGAAATTCAGAGAGAGAGAGAAATTC 395
Db 288 CCAAGAGCGGAGCAGAGCGCCAAAGAGGAGAAATTCAGAGAGAGAGAGAAATTC 347
Qy 396 GAAAGGAGAGAGAAATTCAGAGCTCTCTCTTGGCTCCAGTGGCTCTGTGGGAGTC 455
Db 348 GAAAGGAGAGAGAAATTCAGAGCTCTCTCTTGGCTCCAGTGGCTCTGTGGGAGTC 407
Qy 456 CCTGTCCAGAGAGAGCTGGCCAGATCTGGAGCAGGTGGAGAGAGAGAGAGAGCTCAT 515
Db 408 CCTGTCCAGAGAGAGCTGGCCAGATCTGGAGCAGGTGGAGAGAGAGAGAGAGCTCAT 467
Qy 516 TCCACAGATCCGAGCAAGCCCTGGCCATGGCAAGAGCTGACAGAGCTCAGGAGGC 575
Db 468 TCCACAGATCCGAGCAAGCCCTGGCCATGGCAAGAGCTGACAGAGCTCAGGAGGC 527
Qy 576 CCAAGAGATTTGGAGAGATGAGAGTGGCTGGGAAAGGGGAAAGCCAGCACTATA 635
Db 528 CCAAGAGATTTGGAGAGATGAGAGTGGCTGGGAAAGGGGAAAGCCAGCACTATA 587
Qy 636 TCCACAGATGCTGATGGCAAGAAATGGGCAAAATTTAAGAGAGCTTTGATAATTT 695
Db 588 TCCACAGATGCTGATGGCAAGAAATGGGCAAAATTTAAGAGAGCTTTGATAATTT 647
Qy 696 CAAAGACTCAATGATCCCTGGGAAATGAGATCAAGAGCAATTTGAAGTCACTTTGGTTC 755
Db 648 CAAAGACTCAATGATCCCTGGGAAATGAGATCAAGAGCAATTTGAAGTCACTTTGGTTC 707
Qy 756 TCAAGTGCATGATTTCACTCTTCTCCAGTGAATGATGAGATTAACCTTGTCTTT 815
Db 708 TCAAGTGCATGATTTCACTCTTCTCCAGTGAATGATGAGATTAACCTTGTCTTT 767
Qy 816 TGGCTAATATTTGGTCTAGTCAATATCCAGAGAGTACTGATGGGATGCCATAGGAG 875
Db 768 TGGCTAATATTTGGTCTAGTCAATATCCAGAGAGTACTGATGGGATGCCATAGGAG 827
Qy 876 TATTCAGAGAGAGAGTGGCTGGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 935
Db 828 TATTCAGAGAGAGAGTGGCTGGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 887
Qy 936 TTGGGATTTTGGGGCTATATCAAGTACTGCACTTTCTATATGGCTACTACAAACA 995
Db 888 TTGGGATTTTGGGGCTATATCAAGTACTGCACTTTCTATATGGCTACTACAAACA 947
Qy 996 GAGAGCAATGGGCTGGCTGAGGCTACGGCTGCCATAGGCTTATATGGTGGGGTCA 1055
Db 948 GAGAGCAATGGGCTGGCTGAGGCTACGGCTGCCATAGGCTTATATGGTGGGGTCA 1007
Qy 1056 CGTGTGGGCTACAGCTCATTTATTCATTCGATGATGAGCAATATCCAGAGAG 1115
Db 1008 CGTGTGGGCTACAGCTCATTTATTCATTCGATGATGAGCAATATCCAGAGAG 1067

QY 1116 CACAGGCGAAGGGAGAGTGAACAATTACATTCAGCTTCAAGATGCTTACAGAGCTGGGA 1175
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Db 1068 CACAGGCGAAGGGAGAGTGAACAATTACATTCAGCTTCAAGATGCTTACAGAGCTGGGA 1127
QY 1176 CTACCTGATCGGAAATTCAGAGACAGCTGATTAACAATATGCATCTACACACAGCTT 1235
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Db 1128 CTACCTGATCGGAAATTCAGAGACAGCTGATTAACAATATGCATCTACACACAGCTT 1187
QY 1236 CAGGAAATCAATAGTGAATGAACAAGAGTAAACAAAGAAAGAAATATCCATCTGACAG 1295
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Db 1188 CAGGAAATCAATAGTGAATGAACAAGAGTAAACAAGAAAGAAATATCCATCTGACAG 1247
QY 1296 ATTTCTGCTGCTCGCCAACTTTCTCATCATCTGCTGTTGTGTGAAGTGGGTACCT 1355
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Db 1248 ATTTCTGCTGCTCGCCAACTTTCTCATCATCTGCTGTTGTGTGAAGTGGGTACCT 1307
QY 1356 CATTTACTTTGTGGTTAAGCAATCTCAGCAATCTCCAAATGCAAGATGTCAAGCTGGTA 1415
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Db 1308 CATTTACTTTGTGGTTAAGCAATCTCAGCAATCTCCAAATGCAAGATGTCAAGCTGGTA 1367
QY 1416 TGAAGGAATGAGGTAGAGATCGTATGTCCTGCTTGGATGTTTGTCCCCCTGCTT 1475
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Db 1368 TGAAGGAATGAGGTAGAGATCGTATGTCCTGCTTGGATGTTTGTCCCCCTGCTT 1427
QY 1476 TGAACCAATGAGTGGCTGGAGAAATTACACCCAGCACTGGAAGTGGCACTGGG 1535
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Db 1428 TGAACCAATGAGTGGCTGGAGAAATTACACCCAGCACTGGAAGTGGCACTGGG 1487
QY 1536 AGCAATCTTTGCACTTCTCGTGGGGAAGCTCTACACAATTTCTTGGCCCTGATGAGTGA 1595
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Db 1488 AGCAATCTTTGCACTTCTCGTGGGGAAGCTCTACACAATTTCTTGGCCCTGATGAGTGA 1547
QY 1596 CGTCACTCTCAAGCTTGCCTAATGAGAGACAATAAGAACATCACTCAGCTGACTGTT 1655
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Db 1548 CGTCACTCTCAAGCTTGCCTAATGAGAGACAATAAGAACATCACTCAGCTGACTGTT 1607
QY 1656 TAACTAATTACAACCTCTCTGGTTGGAACGAGAGTGTCCCCGACACCCCTGACCTGC 1715
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Db 1608 TAACTAATTACAACCTCTCTGGTTGGAACGAGAGTGTCCCCGACACCCCTGACCTGC 1667
QY 1716 AGATGTCGCCCGGGGTCTTGTCTGGGAGACAGCTGTGGGCAATGAAATTCATGAGGCTGAC 1775
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Db 1668 AGATGTCGCCCGGGGTCTTGTCTGGGAGACAGCTGTGGGCAATGAAATTCATGAGGCTGAC 1727
QY 1776 GGTGTCTGACATGCTGCTGATACGTACATCACCAATCTGCTGGGGGACCTTCTTAAGGGCTTG 1835
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Db 1728 GGTGTCTGACATGCTGCTGATACGTACATCACCAATCTGCTGGGGGACCTTCTTAAGGGCTTG 1787
QY 1836 TTTTGTGGGTTCAAGAACTACTGCTGGTGGCTGGGACTTGAAGGCTGAAATTCCTCAATA 1895
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Db 1788 TTTTGTGGGTTCAAGAACTACTGCTGGTGGCTGGGACTTGAAGGCTGAAATTCCTCAATA 1847
QY 1896 TGCTGAGTTGATATTAGTGAAGATGCTGGGTTGATCTTCAACCAAGAAATGATCTG 1955
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Db 1848 TGCTGAGTTGATATTAGTGAAGATGCTGGGTTGATCTTCAACCAAGAAATGATCTG 1907

QY 1956 GATGGGCTCCTTCTATGCTCAAGGCTGTGGGCAATTAAATGCTGCGGCTGCTGACTTC 2015
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Db 1908 GATGGGCTCCTTCTATGCTCAAGGCTGTGGGCAATTAAATGCTGCGGCTGCTGACTTC 1967
QY 2016 CATGTACTTCAGTGTCTGGGCGGTGATGACAGCAAAAGCTACCCCATGAAGGCGTGTCAA 2075
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Db 1968 CATGTACTTCAGTGTCTGGGCGGTGATGACAGCAAAAGCTACCCCATGAAGGCGTGTCAA 2027
QY 2076 AGCCTCCGATCCAAACAATTCTACATGGGCTCTGCTGCTGGTGTCTTCTCAAGCCT 2135
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Db 2028 AGCCTCCGATCCAAACAATTCTACATGGGCTCTGCTGCTGGTGTCTTCTCAAGCCT 2087
QY 2136 CCTGCCGTGGGCTTACACATCAATGTCCCTCCCACTCTCTTGACTGGGGGCGTTCAAG 2195
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Db 2088 CCTGCCGTGGGCTTACACATCAATGTCCCTCCCACTCTCTTGACTGGGGGCGTTCAAG 2147
QY 2196 TGGGAAAACAGATGTAAGATGTCTCTCAAGAGACATGTAAGAAAGATTTCCAACTT 2255
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Db 2148 TGGGAAAACAGATGTAAGATGTCTCTCAAGAGACATGTAAGAAAGATTTCCAACTT 2207
QY 2256 CCTGGGCAAGATCTTTGCTTCCCTGCCAATCCAGGCTGATCATCCAGCACTCTGCT 2315
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Db 2208 CCTGGGCAAGATCTTTGCTTCCCTGCCAATCCAGGCTGATCATCCAGCACTCTGCT 2267
QY 2316 GATGTTCTGGGCAATTTACTACCTGAACCTAGTTTCCAAAAGCCTTTCCGAGCTAATGC 2375
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Db 2268 GATGTTCTGGGCAATTTACTACCTGAACCTAGTTTCCAAAAGCCTTTCCGAGCTAATGC 2327
QY 2376 CCAAGTCAAGGAAGAAATCCAAAGTGTCTCGTGAAGTGAAGAGTCAAAATCTGTAAA 2435
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Db 2328 CCAAGTCAAGGAAGAAATCCAAAGTGTCTCGTGAAGTGAAGAGTCAAAATCTGTAAA 2387
QY 2436 AGGCAAGCCACAGGCCAGAGATTCAAGAGACACACTAAAGCACTCCAAAATGSCAC 2495
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Db 2388 AGGCAAGCCACAGGCCAGAGATTCAAGAGACACACTAAAGCACTCCAAAATGSCAC 2447
QY 2496 CCAAGTCAAGTCAAGGAAGAGACACTCTGCTGCTGCTGCAAGCAAGCAGGCACT 2555
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Db 2448 CCAAGTCAAGTCAAGGAAGAGACACTCTGCTGCTGCTGCAAGCAAGCAGGCACT 2507
QY 2556 GGAAGAAAGGGCGAGGGGCTGGGACCTCAAAATCTGCCAGAGGACCAACACTGCTGCG 2615
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Db 2508 GGAAGAAAGGGCGAGGGGCTGGGACCTCAAAATCTGCCAGAGGACCAACACTGCTGCG 2567
QY 2616 CTCTGACACACTTCTATATCTCGGCCCCCTGGAAATGGAACCAAGATTCTGGCAGCGCCC 2675
|||||
Db 2568 CTCTGACACACTTCTATATCTCGGCCCCCTGGAAATGGAACCAAGATTCTGGCAGCGCCC 2627
QY 2676 ATCTCAGACTCATCCGTGAAGGTCAAGCTCTGGAAGAGTGTCTCAGAGACCTCCCACTG 2735
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Db 2628 ATCTCAGACTCATCCGTGAAGGTCAAGCTCTGGAAGAGTGTCTCAGAGACCTCCCACTG 2687
QY 2736 ACGGCTAGGACTCCAGGGAAGCCTCGACCTAGGGGCTGATCTCAAGTACCCGAGTTTCA 2795
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Db 2688 ACGGCTAGGACTCCAGGGAAGCCTCGACCTAGGGGCTGATCTCAAGTACCCGAGTTTCA 2747
QY 2796 ACATACCAACCAAGTTCTCTCCCTCTTCTCTCAGATACATGCTCTGCTCTC 2855

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Db 2748 ACATACCAACCAAGGTTCTCTCCCTCTTCTCTCATATCATGCTGTCTCTCTC 2807
QY 2856 TTGGAATGCATGAACTTGATTCTCTCAAGCCCTTGTCAAGTACCGAAGGAAGACAG 2915
Db 2808 TTGGAATGCATGAACTTGATTCTCTCAAGCCCTTGTCAAGTACCGAAGGAAGACAG 2867
QY 2916 TGGCTTCACTGTCTTTAGGAAGCTGAGGCATCTGCACTAACTGCCCTCCCAAT 2975
Db 2868 TGGCTTCACTGTCTTTAGGAAGCTGAGGCATCTGCACTAACTGCCCTCCCAAT 2927
QY 2976 ATCTTGTTCAGACAGCTCTGAACCCAGCTCAAGTGGTGAACCTTGGCTCCGATT 3035
Db 2928 ATCTTGTTCAGACAGCTCTGAACCCAGCTCAAGTGGTGAACCTTGGCTCCGATT 2987
QY 3036 TCGAGATTGGGGAAGGGCCATGACACCCCTGTTAGACTTTTCCATGGATACAGTTTAA 3095
Db 2988 TCGAGATTGGGGAAGGGCCATGACACCCCTGTTAGACTTTTCCATGGATACAGTTTAA 3047
QY 3096 GACACGGGTTTCTGCCAGCTTCCCTAACAGAGAGGGGATGGAGAGGGCTACATTTCT 3155
Db 3048 GACACGGGTTTCTGCCAGCTTCCCTAACAGAGAGGGGATGGAGAGGGCTACATTTCT 3107
QY 3156 CATTCCAGAGGAAG 3169
Db 3108 CATTCCAGAGGAAG 3121

RESULT 3
US-10-450-763-28100
; Sequence 28100, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: HySeq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 28100
; LENGTH: 5027
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1906)..(2340)
; OTHER INFORMATION: 100% homologous to Homo sapiens d3686c3.3 (novel
; OTHER INFORMATION: gene), accession number AL049712, Smith-Waterman Score=778.
US-10-450-763-28100

Query Match 55.2%; Score 1750; DB 9; Length 5027;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1750; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 947 AGGGCTATATCAAGTCTGGACCTCTTCTATGGCTACTGACCAACAGAGACCATCG 1006
Db 1094 AGGGCTATATCAAGTCTGGACCTCTTCTATGGCTACTGACCAACAGAGACCATCG 1153
QY 1007 GGTGGCTGAGGTACCGGCTGCTATGGCTTACTTATGGTGGGGGTCAAGCTGTTCGGCT 1066
Db 1154 GGTGGCTGAGGTACCGGCTGCTATGGCTTACTTATGGTGGGGGTCAAGCTGTTCGGCT 1213
QY 1067 AAGCTGATTTATGTCAATTCATGCATGGCCAGCAATACCAAGAGACAGGGGAAG 1126
Db 1214 AAGCTGATTTATGTCAATTCATGCATGGCCAGCAATACCAAGAGAGAGAGGGAAG 1273
QY 1127 GGAAGGTGACAACTTCACTTCAAGTGTGACCACTGGGACTACCTGATCG 1186
Db 1274 GGAAGGTGACAACTTCACTTCAAGTGTGACCACTGGGACTACCTGATCG 1333
QY 1187 GGAATTGAGACAGCTGATTAACAAATATGCAATCAGCAACAGCTTCAAGGATCA 1246
Db 1334 GGAATTGAGACAGCTGATTAACAAATATGCAATCAGCAACAGCTTCAAGGATCA 1393
QY 1247 TAGTGGATGAAGAGAGGTACCAAGAAATATCATCTGACAGATTTCTTCGTG 1306
Db 1394 TAGTGGATGAAGAGAGGTACCAAGAAATATCATCTGACAGATTTCTTCGTG 1453
QY 1307 TCGTGGCCAACTTTCTCATCATCTGCTGTTGTGGAAAGGGGTACCTTACTTTTG 1366
Db 1454 TCGTGGCCAACTTTCTCATCATCTGCTGTTGTGGAAAGGGGTACCTTACTTTTG 1513
QY 1367 TGGTTAAGCAATCTCAACAAATTCGCAAAATGCAAGATGCACTGATGAAGGAATG 1426
Db 1514 TGGTTAAGCAATCTCAACAAATTCGCAAAATGCAAGATGCACTGATGAAGGAATG 1573
QY 1427 AAGTAAAGATCGTGAATGCCGTGGTGGAAATGTTTTGCCCCCTCTGTTTGAACCATCG 1486
Db 1574 AAGTAAAGATCGTGAATGCCGTGGTGGAAATGTTTTGCCCCCTCTGTTTGAACCATCG 1633
QY 1487 CTGGCCGGAAGAAATTAACACCAAGCACTGGAATGAGTGGAGCTGGGAGCATCTTG 1546
Db 1634 CTGGCCGGAAGAAATTAACACCAAGCACTGGAATGAGTGGAGCTGGGAGCATCTTG 1693
QY 1547 CACTCTTCTGGGAAACCTCTACACATTTCTTGGCCCTGATGATGAACGTCACCTCA 1606
Db 1694 CACTCTTCTGGGAAACCTCTACACATTTCTTGGCCCTGATGATGAACGTCACCTCA 1753
QY 1607 AGCTTGTATGAAGACATTAAGAACTCACTCACTGGAATCTGTTTAAGTATTACA 1666
Db 1754 AGCTTGTATGAAGACATTAAGAACTCACTCACTGGAATCTGTTTAAGTATTACA 1813
QY 1667 ACTCTTCTGGTTGAAGAGAGGTGCCCGACCAACCCCTGCAACCTGAGATGTCGCC 1726
Db 1814 ACTCTTCTGGTTGAAGAGAGGTGCCCGACCAACCCCTGCAACCTGAGATGTCGCC 1873
QY 1727 GGGGTTCTTGTGGAGAGACGCTGTGGGCAATTGAATTCAAGGCTGACGGTGTCTACA 1786

Db 1874 GGGGTTCTTGCTGGGAGACAGCTGTGGGCAATTGAATTCATGAGGTGACGGTGTCTGACA 1933
QY 1787 TGGTGGTAAGTACATCAACATCCCTGGTGGGAGCTTCCTACGGGCTGTGTTTGCGGGT 1846
Db 1934 TGGTGGTAAGTACATCAACATCCCTGGTGGGAGCTTCCTACGGGCTGTGTTTGCGGGT 1993
QY 1847 TCATGAAGTACTGCTGGTGGTGGGACTTGGAGGCTGGATTTCTCTCAATATGCTGAGTTTG 1906
Db 1994 TCATGAAGTACTGCTGGTGGTGGGACTTGGAGGCTGGATTTCTCTCAATATGCTGAGTTTG 2053
QY 1907 ATATTAAGGAATGCTGGGTTGATCTTCACCAAGAAATGATCTGGATGGGCTCT 1966
Db 2054 ATATTAAGGAATGCTGGGTTGATCTTCACCAAGAAATGATCTGGATGGGCTCT 2113
QY 1967 TCTATGCTCGAGGCTGGTGGGCAATTAATGCTGGGCTGGTGAAGCTCCATGTACTTC 2026
Db 2114 TCTATGCTCGAGGCTGGTGGGCAATTAATGCTGGGCTGGTGAAGCTCCATGTACTTC 2173
QY 2027 AGTGTGGGCGGTGATGACAGCAAGTACCCCATGAAGCGGTGTTCAAGGCTCCCGAT 2086
Db 2174 AGTGTGGGCGGTGATGACAGCAAGTACCCCATGAAGCGGTGTTCAAGGCTCCCGAT 2233
QY 2087 CCAAGCACTTCTAATGGGCTCTGCTGTGTGCTCTTCTCAAGCTCTGCGGGTGG 2146
Db 2234 CCAAGCACTTCTAATGGGCTCTGCTGTGTGCTCTTCTCAAGCTCTGCGGGTGG 2293
QY 2147 CTAACACCATCATGTCCTCCACCCCTCTTGACTGCGGGCGGTGATGGGAAAAACA 2206
Db 2294 CTAACACCATCATGTCCTCCACCCCTCTTGACTGCGGGCGGTGATGGGAAAAACA 2353
QY 2207 GAATGTACGATGCTCCAGAGACCAATGAAAAAGATTTCCAACTTCTGGGCAAGA 2266
Db 2354 GAATGTACGATGCTCCAGAGACCAATGAAAAAGATTTCCAACTTCTGGGCAAGA 2413
QY 2267 TCTTGGCTTCTCGCAATCCAGGCTGATCATCCAGCAATCTGCTGATGTTCTTGG 2326
Db 2414 TCTTGGCTTCTCGCAATCCAGGCTGATCATCCAGCAATCTGCTGATGTTCTTGG 2473
QY 2327 CCATTTACTACTGAAGTCAATTCMAAGGCTTTCCGAGCTAATGCCAGCTGAGGA 2386
Db 2474 CCATTTACTACTGAAGTCAATTCMAAGGCTTTCCGAGCTAATGCCAGCTGAGGA 2533
QY 2387 AGAAAAATCCAAAGTCTCCGTGAAGTTGAGAGAGTCACAATCTGTAAAAAGCAAGCA 2446
Db 2534 AGAAAAATCCAAAGTCTCCGTGAAGTTGAGAGAGTCACAATCTGTAAAAAGCAAGCA 2593
QY 2447 CAGCGAGAGTCAAGAGAGACCACTTAAGAGAGCTGCAAAATGGCAAGCTCCAGC 2506
Db 2594 CAGCGAGAGTCAAGAGAGACCACTTAAGAGAGCTGCAAAATGGCAAGCTCCAGC 2653
QY 2507 TCACCAAGAGAGAGCACTCTCCCTGTCACAGCAAGCCAGGCTTGAACAAGAG 2566
Db 2654 TCACCAAGAGAGAGAGCACTCTCCCTGTCACAGCAAGCCAGGCTTGAACAAGAG 2713
QY 2567 CCGAGGCGCTGGAGCTCCAAATTCGCAAGAGAGACCAAGCTGCTGCTGAGACCC 2626

Db 2714 CCGAGGCGCTGGAGCTCCAAATTCGCAAGAGAGACCAAGCTGCTGCTGAGACCC 2773
QY 2627 TTCTATATATCTGGGCGCCCTGGAATCGAGCAAGATCTGGGCAAGCCCATCTCAGACTC 2686
Db 2774 TTCTATATATCTGGGCGCCCTGGAATCGAGCAAGATCTGGGCAAGCCCATCTCAGACTC 2833
QY 2687 ATCCGTGAG 2696
Db 2834 ATCCGTGAG 2843

RESULT 4
US-10-115-831-134
; Sequence 134, Application US/10115831
; Publication No. US20030219743A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyen
; APPLICANT: Drmanac, Radraje T.
; TITLE OF INVENTION: No. US20030219743A1el Nucleic Acids and
; FILE REFERENCE: 792CIP2ADIV
; CURRENT APPLICATION NUMBER: US/10/115,831
; PRIOR APPLICATION NUMBER: 2002-04-02
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: pc_fl_genes Version 2.0
; SEQ ID NO 134
; LENGTH: 4895
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4785)
US-10-115-831-134

Query Match 52.0%; Score 1648; DB 6; Length 4895;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1748; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 947 AGGGCTATATCAAGTACTGCACTTTCTATGGCTACTACAAACAGAGACATCG 1006
Db 1094 AGGGCTATATCAAGTACTGCACTTTCTATGGCTACTACAAACAGAGACATCG 1153
QY 1007 GGTGGCTGAGGATCCGGCTGCTATGGCTTAAGTTATGGTGGGGTCAAGCTGTTGGCT 1066
Db 1154 GGTGGCTGAGGATCCGGCTGCTATGGCTTAAGTTATGGTGGGGTCAAGCTGTTGGCT 1213
QY 1067 AAGGCTGATTATGTCAATTCATGATGGCAGCAATACCAAGAGAGCAAGAGGAG 1126
Db 1214 AAGGCTGATTATGTCAATTCATGATGGCAGCAATACCAAGAGAGAGGAGAG 1273

| | | | |
|----|------|--|------|
| Db | 2114 | TCGATGCTCCAGGGCTGGTGGGCATTAATGTGTGGGCGCTGGTGAAGCTCATGTACTCTG | 2173 |
| QY | 2027 | AAGTGGGGGGGGGTGATGAGCAGCAAGTACCCCATGAAAGCGTGTTCAAAGCTTCCCGAT | 2086 |
| Db | 2174 | AAGTGGTGGGGGGGTGATGAGCAGCAACCTACCCCATGAAAGCGTGTTCAAAGCGTCCCGAT | 2233 |
| QY | 2087 | CCAAACAATTCATCAATGGGCGCTCGTGGTGGTGGTCTTCCAGAGCTCGTGGCGGGTGG | 2146 |
| Db | 2234 | CCAAACAATTCATCAATGGGCGCTCGTGGTGGTGGTCTTCCAGAGCTCGTGGCGGGTGG | 2293 |
| QY | 2147 | CCCAACACATCATGTCCCTCCCAAGCGCTTCTGATGTGGGGGGCGCTTCAAGTGGAAAAACA | 2206 |
| Db | 2294 | CCCAACACATCATGTCCCTCCCAAGCGCTTCTGATGTGGGGGGCGCTTCAAGTGGAAAAACA | 2353 |
| QY | 2207 | GAAATGTACATGTCTCTCAAGAGACATTTGAAAAACATTTCCCAAGCTTCTGGGCAAA | 2266 |
| Db | 2354 | GAAATGTACATGTCTCTCAAGAGACATTTGAAAAACATTTCCCAAGCTTCTGGGCAAA | 2413 |
| QY | 2267 | TCTTTGGTCTTCTCGCCATCCAGGCGCTGATCATCCAGCCATCTGTGCTGATGTTCTTGG | 2326 |
| Db | 2414 | TCTTTGGTCTTCTCGCCATCCAGGCGCTGATCATCCAGCCATCTGTGCTGATGTTCTTGG | 2473 |
| QY | 2327 | CCATTTACTACCTGAAGCTCAAGTTTCCAAAAGCCTTTCGAGAGTAAAGCCAGCTGAAGA | 2386 |
| Db | 2474 | CCATTTACTACCTGAAGCTCAAGTTTCCAAAAGCCTTTCGAGAGTAAAGCCAGCTGAAGA | 2533 |
| QY | 2387 | AAGAAATCCCAATGCTGCTCCGTGAAGTGAAGAGATCAAAATCTTAAAGGCAAAAGCA | 2446 |
| Db | 2534 | AAGAAATCCCAATGCTGCTCCGTGAAGTGAAGAGATCAAAATCTTAAAGGCAAAAGCA | 2593 |
| QY | 2447 | CAGCGAGAGATTTCAGAGGACACACCTTAAAGCAGCTCCAAAAATGCCACCAAGCTCCAA | 2506 |
| Db | 2594 | CAGCGAGAGATTTCAGAGGACACACCTTAAAGCAGCTCCAAAAATGCCACCAAGCTCCAA | 2653 |
| QY | 2507 | TCAACCAAGAAAGACACATCTCTCCCTGTGCACCAAGGCGACGATGACAAAGAG | 2566 |
| Db | 2654 | TCAACCAAGAAAGACACATCTCTCCCTGTGCACCAAGGCGACGATGACAAAGAG | 2713 |
| QY | 2657 | CGCAGGGGCGCTGGAGCTCCAAATCTTGCACGAGGAGACACACTGCTGCTGTGGAACG | 2626 |
| Db | 2714 | CGCAGGGGCGCTGGAGCTCCAAATCTTGCACGAGGAGACACACTGCTGCTGTGGAACG | 2773 |
| QY | 2627 | TTCCATATATCTGGGCGCCCTGGAATGGAGACAGATCTGGACAGGCCCATCTCAGACTC | 2686 |
| Db | 2774 | TTCCATATATCTGGGCGCCCTGGAATGGAGACAGATCTGGACAGGCCCATCTCAGACTC | 2833 |
| QY | 2687 | ATTCGTGGAG 2696 | |
| Db | 2834 | ATTCGTGGAG 2843 | |

Qy 1907 ATATTAGTGAATGCTGGGTTATCTTCAACAGAAATGATGATGGGCTCC 1966
 |||||
 Db 2054 ATATTAGTGAATGCTGGGTTATCTTCAACAGAAATGATGATGGGCTCC 2113
 |||||
 Qy 1967 TCTATGCTCAAGGCTGGTGGGCACTTAATGCTGGGCGCTGCTCACTCATGTAATTCC 2026
 |||||

RESULT 5
 US-10-108-260A-342
 ; Sequence 342, Application US/10108260A
 ; Publication No. US20040005560A1
 ; GENERAL INFORMATION:

| | | | | |
|-----------------------|--------------|---------------------|---------------|--------------|
| Query Match | 15.6%; | Score 493; | DB 6; | Length 2560; |
| Best Local Similarity | 99.7%; | Pred. No. 1.2e-252; | | |
| Matches 593; | Conservative | 0; | Mismatches 2; | Indels 0; |
| | | | | Gaps 0; |

| | | | |
|----|------|---|------|
| QY | 1293 | AAGATTTCCTCGGTCCGGCCAACTTTCATCATCTGCTGTTTGTCTGGAAAGTGGGTA | 135 |
| Db | 1 | AAATATTCCTCGGTCCGGCCAACTTTCATCATCTGCTGTTTGTCTGGAAAGTGGGTA | 60 |
| QY | 1353 | CCTCATTTACTTGTGGTTAAGCATCTCAGCAATTTCTCCAAAATGCAGATGTCAAGCTG | 1412 |
| Db | 61 | CCCATTTACTTGTGGTTAAGCATCTCAGCAATTTCTCCAAAATGCAGATGTCAAGCTG | 120 |
| QY | 1413 | GTATGAAAGGATGAGGTAAAGATCTGTGATGTCTCTGCTTGGAAATGTTTGTGCCCCCTCT | 1472 |
| Db | 121 | GTATGAAAGGATGAGGTAAAGATCTGTGATGTCTCTGCTTGGAAATGTTTGTGCCCCCTCT | 180 |
| QY | 1473 | GTTTGAAACCAATGCGTGGCCTGGAGAAATTCACACCACGACATGAGATGGAGCAACT | 1533 |
| Db | 181 | GTTTGAAACCAATGCGTGGCCTGGAGAAATTCACACCACGACATGAGATGGAGCAACT | 240 |
| QY | 1533 | GGGACGCACTTTGGCACTCTTCTGCGGGAACCTCTACACATTTCTTGGCCTCATGGA | 1592 |
| Db | 241 | GGGACGCACTTTGGCACTCTTCTGCGGGAACCTCTACACATTTCTTGGCCTCATGGA | 300 |
| QY | 1593 | TGACGTCGACGCTCAAGCTTCTCTAATGAAGAGACATTAAGAACATCACTCACTGGACTCT | 1652 |
| Db | 301 | TGATGTCGACGCTCAAGCTTCTCTAATGAAGAGACATTAAGAACATCACTCACTGGACTCT | 360 |
| QY | 1653 | GTTTTAACATTACAACCTCTTCTGTGTGGAAAGAGATGTCCCCCAACAACCCCTGCAACC | 1712 |
| Db | 361 | GTTTTAACATTACAACCTCTTCTGTGTGGAAAGAGATGTCCCCCAACAACCCCTGCAACC | 420 |
| QY | 1713 | TGCAAGATGTCCCGCGGGGTTCTTCTGTGGAGACAGCTGTGGGCAATGAATTCAGAGGCT | 1772 |
| Db | 421 | TGCAAGATGTCCCGCGGGGTTCTTCTGTGGAGACAGCTGTGGGCAATGAATTCAGAGGCT | 480 |
| QY | 1773 | GACGGGTGTGACATGCTGGTTAAGCTACATCAACAATCTCTGTGGGGACTTCTACGGGGC | 1832 |
| Db | 481 | GACGGGTGTGACATGCTGGTTAAGCTACATCAACAATCTCTGTGGGGACTTCTACGGGGC | 540 |
| QY | 1833 | TTGCTTTGTGCGGTTCAATGAAGTACTGCTGTGGTGGGACTTGGAGCTGTGAATTA | 1887 |
| Db | 541 | TTGCTTTGTGCGGTTCAATGAAGTACTGCTGTGGTGGGACTTGGAGCTGTGAATTA | 595 |

Query Match 4.8%; Score 153; DB 5; Length 1060;
Best Local Similarity 100.0%; Pred. No. 2e-70;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

RESULT 7
US-10-027-632-122322/c
; Sequence 123322, Application US/100276322
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; PRIOR FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 122322
;; LENGTH: 1060
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-122322

Query Match 4.8%; Score 153; DB 6; Length 1060;
Best Local Similarity 100.0%; Pred. No. 2e-70;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1607 ACCTTGCTAATGAAGACAAATMAAGACATCACTGAGCTGTGTTAATTACCA 1666
Db 671 ACCTTGCTAATGAAGACAAATMAAGACATCACTGAGCTGTGTTAATTACCA 612
QY 1667 ACTCTCTGCTGGGAACGAGAGTCCGCCGACCACTGACCTGGACCTGGAGTGGCCC 1726
Db 611 ACTCTCTGCTGGGAACGAGAGTCCGCCGACCACTGACCTGGAGTGGCCC 552
QY 1727 GGGGTTCTGCTGGGAGACAGCTGTGGCATTG 1759
Db 551 GGGGTTCTGCTGGGAGACAGCTGTGGCATTG 519

Search completed: December 6, 2005, 04:45:10
Job time : 2438 secs

OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 12:30:06 ; Search time 499 Seconds
(without alignments)
1976.466 Million cell updates/sec

Title: US-10-792-307-3
Percent score: 3169
Sequence: 1 gcagtgctgctgacatgag.....attccatccagaggaag 3169

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 328935 seqs, 155610033 residues

Word size : 110

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications_NA_New:*

| | |
|-----|--|
| 1: | /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:* |
| 2: | /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:* |
| 3: | /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:* |
| 4: | /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:* |
| 5: | /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:* |
| 6: | /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:* |
| 7: | /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:* |
| 8: | /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:* |
| 9: | /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:* |
| 10: | /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:* |

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Query | Score | Match | Length | ID | Description |
|------------------|-------|-------|-------|--------|----|-------------|
| No matches found | | | | | | |

Search completed: December 6, 2005, 04:04:22
Job time : 499 secs

Db 1099 CTGACCTTCATGCTACTTCACGTCTGGGGGCTGATGAGAGCAAGTACCCATTGAACGC 1158

QY 2068 GTGTTCAAAGCCTCCCGATCCAAACAATTCTACATGGAGCTCTGCTGCTGGTGTTC 2127

Db 1159 GTGTTCAAAGCCTCCCGATCCAAACAATTCTACATGGAGCTCTGCTGCTGGTGTTC 1218

QY 2128 CTGACCTCTGCTGGGCTGGCTTACACATTCATGTCCTCCCACTCTCTTTGACTGGGAG 2187

Db 1219 CTGACCTCTGCTGGGCTGGCTTACACATTCATGTCCTCCCACTCTCTTTGACTGGGAG 1278

QY 2188 CCGTTCAG 2195

Db 1279 CCGTTCAG 1286

RESULT 2

LOCUS CD635963 247 bp mRNA linear EST 12-JAN-2004

DEFINITION 56089332H1 FLP Homo sapiens cDNA, mRNA sequence.

ACCESSION CD635963

VERSION CD635963.1 GI:40284230

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 247)

AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.

TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes

JOURNAL Genomics 84 (1), 205-210 (2004)

PUBMED 15203218

COMMENT

Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES

source Location/Qualifiers

1..247

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_lib="FLP"

/note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 7.6%; Score 241; DB 6; Length 247;

Best Local Similarity 100.0%; Pred. No. 3e-113; Mismatches 0; Indels 0; Gaps 0;

Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1095 GGCCAGCAATACCCAGGAAGCAAGGCGAAGGGAGAGTGAACAATTCACTTCAAGCTT 1154

Db 7 GGCCAGCAATACCCAGGAAGCAAGGCGAAGGGAGAGTGAACAATTCACTTCAAGCTT 66

QY 1155 CAAGATGTTCAACCACTGGGACTACCTGATCGGAATTCAAGACAGCTGATTAACAATA 1214

Db 67 CAAGATGTTCAACCACTGGGACTACCTGATCGGAATTCAAGACAGCTGATTAACAATA 126

QY 1215 TGCATTCATCACACACAGCTTCAGAGAAATCAATAGTGAATGAACAGAGATTAACAAGA 1274

Db 127 TGCATTCATCACACACAGCTTCAGAGAAATCAATAGTGAATGAACAGAGATTAACAAGA 186

QY 1275 AGAAATAATTCATCTGACAAAGATTCTTCCTGCTGGCCAACTTTCTCATCATCTGCTG 1334

Db 187 AGAAATAATTCATCTGACAAAGATTCTTCCTGCTGGCCAACTTTCTCATCATCTGCTG 246

QY 1335 T 1335

Db 247 T 247

RESULT 3

LOCUS CD635964/c 247 bp mRNA linear EST 12-JAN-2004

DEFINITION 56089332J1 FLP Homo sapiens cDNA, mRNA sequence.

ACCESSION CD635964

VERSION CD635964.1 GI:40284231

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 247)

AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.

TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes

JOURNAL Genomics 84 (1), 205-210 (2004)

PUBMED 15203218

COMMENT

Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES

source Location/Qualifiers

1..247

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_lib="FLP"

/note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 7.6%; Score 241; DB 6; Length 247;

Best Local Similarity 100.0%; Pred. No. 3e-113; Mismatches 0; Indels 0; Gaps 0;

Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1095 GGCCAGCAATACCCAGGAAGCAAGGCGAAGGGAGAGTGAACAATTCACTTCAAGCTT 1154

Db 241 GGCCAGCAATACCCAGGAAGCAAGGCGAAGGGAGAGTGAACAATTCACTTCAAGCTT 182

QY 1155 CAAGATGTTCAACCACTGGGACTACCTGATCGGAATTCAAGACAGCTGATTAACAATA 1214

```
Db      181  CAAGATGTTCAACCACTGGGACTACCTGATCGGGAATTCAGAGACAGCTGATTAACAATA 122
QY      1215  TGCATCCATCACCAACAGCTTCAAGGAATCAATAGTGAAGTGAACAGAGTAAACAAGA 1274
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121  TGCATCCATCACCAACAGCTTCAAGGAATCAATAGTGAAGTGAACAGAGTAAACAAGA 62
QY      1275  AGAAATATTCATCTGAACAAGATTCTTCGTCTGGCCAACTTCTCATCATCTGCTG 1334
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  AGAAATATTCATCTGAACAAGATTCTTCGTCTGGCCAACTTCTCATCATCTGCTG 2
QY      1335  T 1335
        |
Db      1  T 1
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Search completed: December 5, 2005, 23:34:52
Job time : 12015 secs

OM nucleic - nucleic search, using sw model

Run on: November 30, 2005, 03:45:30 ; Search time 15410 Seconds
(without alignments)

11689.610 Million cell updates/sec

Title: US-10-792-307-3

Perfect score: 3169

Sequence: 1 gcagtcgtcgtaccatgag.....attctcatccagaggag 3169

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 2842172563 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:.*
1: gb_ba:.*
2: gb_in:.*
3: gb_env:.*
4: gb_sm:.*
5: gb_ov:.*
6: gb_pat:.*
7: gb_ph:.*
8: gb_pr:.*
9: gb_ro:.*
10: gb_sta:.*
11: gb_sy:.*
12: gb_un:.*
13: gb_vt:.*
14: gb_htg:.*
15: gb_pl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | | | | |
|------------|--------|-------|--------|------------|
| Result No. | Score | Match | Length | DB ID |
| 1 | 3169 | 100.0 | 3169 | 8 AF417580 |
| 2 | 1957.6 | 61.8 | 3216 | 9 AF417581 |

| | | | | | | |
|----|--------|------|--------|----|-----------|-----------------------|
| 3 | 131.3 | 41.4 | 3066 | 5 | AY581309 | AY581309 Gallus ga |
| 4 | 1018.2 | 32.1 | 1977 | 5 | AY263168 | AY263168 Takifugu |
| 5 | 943 | 29.8 | 2566 | 5 | AY581308 | AY581308 Gallus ga |
| 6 | 838.8 | 26.5 | 2871 | 5 | AY263167 | AY263167 Takifugu |
| 7 | 816.8 | 25.8 | 2895 | 9 | AF417579 | AF417579 Mus muscu |
| 8 | 814.2 | 25.7 | 3201 | 8 | AF417578 | AF417578 Homo sapi |
| 9 | 651.4 | 20.6 | 159272 | 8 | HSDD686C3 | AL049712 Human DNA |
| 10 | 591.8 | 18.7 | 2560 | 6 | AK833218 | AK833218 Sequence |
| 11 | 591.8 | 18.7 | 2560 | 8 | AK094789 | AK094789 Homo sapi |
| 12 | 462.2 | 14.6 | 6222 | 8 | AY263157 | AY263157 Mus muscu |
| 13 | 456.2 | 14.4 | 4746 | 8 | AY263163 | AY263163 Homo sapi |
| 14 | 444.8 | 14.0 | 2442 | 8 | AY236490 | AY236490 Homo sapi |
| 15 | 443.8 | 14.0 | 3495 | 5 | AY381310 | AY381310 Gallus ga |
| 16 | 441.2 | 13.9 | 3621 | 9 | AY236491 | AY236491 Mus muscu |
| 17 | 374.2 | 11.8 | 884 | 6 | CQ728483 | CQ728483 Sequence |
| 18 | 341.2 | 10.8 | 418 | 9 | AY263156 | AY263156 Mus muscu |
| 19 | 319.4 | 10.1 | 2572 | 2 | AY263175 | AY263175 Anopheles |
| 20 | 308.6 | 9.7 | 3566 | 6 | CQ850588 | CQ850588 Sequence |
| 21 | 308.6 | 9.7 | 3566 | 8 | AK127751 | AK127751 Homo sapi |
| 22 | 296.2 | 9.3 | 1548 | 5 | AY263169 | AY263169 Takifugu |
| 23 | 258.6 | 8.2 | 245113 | 14 | AC156927 | AC156927 Bos tauru |
| 24 | 245.8 | 7.8 | 410 | 9 | AY263155 | AY263155 Mus muscu |
| 25 | 232 | 7.3 | 2276 | 6 | CQ734586 | CQ734586 Sequence |
| 26 | 228.4 | 7.2 | 1528 | 8 | AK098607 | AK098607 Homo sapi |
| 27 | 212 | 6.7 | 200521 | 9 | AL833804 | AL833804 Mouse DNA |
| 28 | 211.8 | 6.7 | 259335 | 14 | AC130173 | AC130173 Rattus nor |
| 29 | 194.2 | 6.1 | 321519 | 14 | AL714004 | AL714004 Homo sapi |
| 30 | 193 | 6.1 | 59229 | 6 | CQ578280 | CQ578280 Sequence |
| 31 | 175.8 | 5.5 | 628 | 10 | BVA16283 | BVA16283 S229P6276 |
| 32 | 172 | 5.4 | 179086 | 5 | BX296526 | BX296526 Zebrafish |
| 33 | 172 | 5.4 | 222623 | 14 | BX502015 | BX502015 Danio rerio |
| 34 | 146.6 | 4.6 | 169358 | 14 | AC163224 | AC163224 Mus musculus |
| 35 | 146.6 | 4.6 | 214117 | 14 | AC162458 | AC162458 Mus musculus |
| 36 | 146.6 | 4.6 | 214504 | 9 | AC102779 | AC102779 Mus muscu |
| 37 | 146.6 | 4.6 | 242249 | 9 | AC102790 | AC102790 Mus muscu |
| 38 | 145.8 | 4.6 | 192769 | 5 | BX571945 | BX571945 Zebrafish |
| 39 | 145.8 | 4.6 | 198392 | 5 | CR383678 | CR383678 Zebrafish |
| 40 | 143.8 | 4.5 | 211075 | 9 | AC076974 | AC076974 Mus muscu |
| 41 | 141.8 | 4.5 | 75609 | 8 | AL162416 | AL162416 Human DNA |
| 42 | 140.2 | 4.4 | 340350 | 14 | AC112299 | AC112299 Rattus nor |
| 43 | 139.8 | 4.4 | 261 | 6 | CQ735558 | CQ735558 Sequence |
| 44 | 126.6 | 4.0 | 222623 | 14 | BX502015 | BX502015 Danio rerio |
| 45 | 126.2 | 4.0 | 129862 | 5 | BX950207 | BX950207 Zebrafish |

ALIGNMENTS

RESULT 1
AF417580
LOCUS AF417580 3169 bp mRNA linear PRI 05-MAR-2003
DEFINITION Homo sapiens transmembrane channel-like protein 2 (TM2) mRNA,
complete cds.
ACCESSION AF417580
VERSION AF417580.2 GI:28642834
KEYWORDS Homo sapiens (human)
SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 3169)
AUTHORS Kurima, K., Peters, L.M., Yang, Y., Riazuddin, S., Ahmed, Z.M., Naz, S.,
Arnaud, D., Drury, S., Mo, J., Makishima, T., Ghosh, M., Menon, P.S.N.,
Deshmukh, D., Oudoux, C., Osterer, H., Khan, S., Riazuddin, S.,
Dehlinger, P.L., Hampton, L.L., Sullivan, S.L., Battey, J.F.,
Keats, B.J.B., Wilcox, E.R., Friedman, T.B. and Griffith, A.J.
Dominant and recessive deafness caused by mutations of a novel
gene, TMCI, required for cochlear hair-cell function
Nat. Genet. 30 (3), 277-284 (2002)
TITLE 2 (bases 1 to 3169)
JOURNAL Kurima, K., Griffith, A.J. and Friedman, T.B.
PUBMED Direct Submission
11850618
REFERENCE 3 (bases 1 to 3169)
AUTHORS Kurima, K., Griffith, A.J. and Friedman, T.B.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-2001) NIDCD, NIH, 5 Research Court, #2N02,
Rockville, MD 20850, USA
REMARK Sequence update by submitter
COMMENT On Mar 3, 2003 this sequence version replaced gi:19223982.
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/map="20p13"
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/gene="TMCI"
16..2736
/gene="TMCI2"
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ERASFGERTAAPKREKEIPRKEEKSRRQKPPRSSSLASXSGEELSSEELAQILEQY
EEKKKLIATMRSKPMPMAKKLELRQAQFVEKYEGALGRGKQQLVAYGLMAKMY
KFKRDEINFTQCIPIWMKIKIDIESHGSSVASYEIFLRMTGNVLVLEGLIGLVII
PEVLKMPYGSIPKTVPRAREEKAMDFAVIMDEFGYIKYSAIFYGYNNORTIGMLR
YRLPAHYMGVSYFGYSLIYVIRSMASNTQSGTGESENFTSEFKRTSMYDLGN
SETADIKRTASTTSFKESIVDQESNKEINHLTRFLRLANFLITCOLGSGTLYIF
VVRSQQFSRMQNVSWERNEVEIVNSLLGNFCPLFETLALENYHRTGLKMQQGR
IFALFLGNLYTFLALADDVHLKLANEETIKNITHMTLFNVSSGNVESVPRPLGR
ADVPRGSCWETAVGIEFMRITVSDMLVYITILLQDFLRACFRRFNYCWMQLEAGF
PSYAEEDISGNVLGITFNGQIMMGFSYAPGAVGNLRLILSNVFOCMVMSNVPH
ERVFRSSNNFYNGILLILVLESLDVAVYATNLSLPSFDCGPESGRRIRYDILDETI
ENDFPTFLGKIFATLANPGLITIPAILNLMEFLAYIYLSVSSCSLRNNAQLKKIQYLRE
VEKSHSVKGRATARDSEDTPRSSSKVAIQQLTKEETTPPSASQAMDKKQAGGT

ORIGIN
SNSASRTTLPA SGHLPLISRP GIGPDSGHAPSQTHTWRSASCKSAQRPHH"
Query Match 100.0%; Score 3169; DB 8; Length 3169;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAGTGGCTGCTGACCATGACCAACAGGTAAAGGCGCTGAAAAGAGACGAGCGGGA 60
|||||
Db 1 GCAGTGGCTGCTGACCATGACCAACAGGTAAAGGCGCTGAAAAGAGACGAGCGGGA 60
QY 61 GTGAAAAGCGCGGCTGAGAGCGGCTCTCCACACACAGTGCACGCTGGGAAAGCATCC 120
|||||
Db 61 GTGAAAAGCGCGGCTGAGAGCGGCTCTCCACACACAGTGCACGCTGGGAAAGCATCC 120
QY 121 TCAGACAAAGCGGCTCTCAAAAGCCAGAGGGAGCCCGACGACGGCGGAGCTCAGGAAAG 180
|||||
Db 121 TCAGACAAAGCGGCTCTCAAAAGCCAGAGGGAGCCCGACGACGGCGGAGCTCAGGAAAG 180
QY 181 CAGAAAGAGGCGCGCGGCGGAGCCCAAGCCCGGGGCTCCCCGAGAGAAAGCAAAACAGG 240
|||||
Db 181 CAGAAAGAGGCGCGCGGCGGAGCCCAAGCCCGGGGCTCCCCGAGAGAAAGCAAAACAGG 240
QY 241 CCGAGAGACACAGAGAAAGCTGGGGAGACAGAGCGGGGCGCAGAGAGAGACTCG 300
|||||
Db 241 CCGAGAGACACAGAGAAAGCTGGGGAGACAGAGCGGGGCGCAGAGAGAGACTCG 300
QY 301 GAGGCGAGAGAAAGCGGACGAGAGGGCGCTCCTCCAGAGGCGACAGCCCCAAAG 360
|||||
Db 301 GAGGCGAGAGAAAGCGGACGAGAGGGCGCTCCTCCAGAGGCGACAGCCCCAAAG 360
QY 361 AGGGAAAGAGAAATTCGAGAGAAAGGAGAAATCGAAGCGGCGAGAAAGCCAGGTCA 420
|||||
Db 361 AGGGAAAGAGAAATTCGAGAGAAAGGAGAAATCGAAGCGGCGAGAAAGCCAGGTCA 420
QY 421 TCCTCTTGGGCTCCAGTGGCTCTGTGGGAGTCCCTGTCCAGAGAGAACTGCCCCAG 480
|||||
Db 421 TCCTCTTGGGCTCCAGTGGCTCTGTGGGAGTCCCTGTCCAGAGAGAACTGCCCCAG 480
QY 481 ATCTGGAGGAGTGAAGAAAGAAAGAAAGTCAATGGCAACATGGGAGCAAGCCCTGG 540
|||||
Db 481 ATCTGGAGGAGTGAAGAAAGAAAGAAAGTCAATGGCAACATGGGAGCAAGCCCTGG 540
QY 541 CCCATGGCGAAGAACTGACAGAGCTCAGGAGGCCCGCAGAAATTTGTGAAGAGTATGAA 600
|||||
Db 541 CCCATGGCGAAGAACTGACAGAGCTCAGGAGGCCCGCAGAAATTTGTGAAGAGTATGAA 600
QY 601 GGTGCTTGGGAAAGGGGAAAGGCAAGCACTATAGCTTACAAAGATGCTGATGGCCAG 660
|||||
Db 601 GGTGCTTGGGAAAGGGGAAAGGCAAGCACTATAGCTTACAAAGATGCTGATGGCCAG 660
QY 661 AAATGGGTCAAAATTAAGAGAGCTTTGATATTTCAAGACTCAAGTATCCCTGGGAA 720
|||||
Db 661 AAATGGGTCAAAATTAAGAGAGCTTTGATATTTCAAGACTCAAGTATCCCTGGGAA 720
QY 721 ATGAAGTCAAGAGCAATTGAAGTCACTTTGGTCTTCAGTGGCATCGATTATTCATCTTT 780
|||||

Db 721 ATGAAGATCAAACAATTGAAAGTCACTTTGGTTCCTCAGTGGCACTGATTTTCATCTTT 780
QY 781 CTCCTGATGATGATGAGATTAACTTTGCTTTTGGCTTAATATTGGCTAGCTATA 840
Db 781 CTCCTGATGATGATGAGATTAACTTTGCTTTTGGCTTAATATTGGCTAGCTATA 840
QY 841 ATCCAGAGGTAGTATGGGCAATGCCCTATGGAGATATCCAGAAAGACAGTCCGCG 900
Db 841 ATCCAGAGGTAGTATGGGCAATGCCCTATGGAGATATCCAGAAAGACAGTCCGCG 900
QY 901 GCTGAGGAAGAAAGGCCATGGAATTTTCTGCTTTGGGATTTTGAAGGCTATATCAAG 960
Db 901 GCTGAGGAAGAAAGGCCATGGAATTTTCTGCTTTGGGATTTTGAAGGCTATATCAAG 960
QY 961 TACTCTGCACCTTCTATGGCTACTACAACAAGAGAACCATCGGCTGGCTGAGGTAC 1020
Db 961 TACTCTGCACCTTCTATGGCTACTACAACAAGAGAACCATCGGCTGGCTGAGGTAC 1020
QY 1021 CGGCTGCCATAGCTTACTTATGGTGGGGGTCAAGCTGTGCGCTCAAGCCTGATTAAT 1080
Db 1021 CGGCTGCCATAGCTTACTTATGGTGGGGGTCAAGCTGTGCGCTCAAGCCTGATTAAT 1080
QY 1081 GTCAATTGATCGATGGCCAGCAATACCAAAGGAACAAGGGGGAAGTGAACA 1140
Db 1081 GTCAATTGATCGATGGCCAGCAATACCAAAGGAACAAGGGGGAAGTGAACA 1140
QY 1141 TTCACATTCAAGCTTCAGATGTTTCAACAAGCTGGGACTACCTGATCGGGAATTCAGAGCA 1200
Db 1141 TTCACATTCAAGCTTCAGATGTTTCAACAAGCTGGGACTACCTGATCGGGAATTCAGAGCA 1200
QY 1201 GCTGATTAACAATATGCAATCCATCAACAACAGCTTCAAGAAATCAATATGAGTAAACA 1260
Db 1201 GCTGATTAACAATATGCAATCCATCAACAACAGCTTCAAGAAATCAATATGAGTAAACA 1260
QY 1261 GAGAGTAAACAAGAAATATCCATCTGACAGATTTCTTCGTCCTGGCCAACTTT 1320
Db 1261 GAGAGTAAACAAGAAATATCCATCTGACAGATTTCTTCGTCCTGGCCAACTTT 1320
QY 1321 CTCATCATCTGCTGTTTGTGTGAAGTGGGTACCTCAATTAATTTGTGTTAAAGCAATC 1380
Db 1321 CTCATCATCTGCTGTTTGTGTGAAGTGGGTACCTCAATTAATTTGTGTTAAAGCAATC 1380
QY 1381 CAGCAATTCTCCAAATGCAAGATGTCAGCTGTGTATGAAAGGAATGAGGTAGAGATGCTG 1440
Db 1381 CAGCAATTCTCCAAATGCAAGATGTCAGCTGTGTATGAAAGGAATGAGGTAGAGATGCTG 1440
QY 1441 ATGTCCCTGCTGGAATGTTTGTCCCTCTGTTTGAAACCATCGCTGCCCTGGAAGAT 1500
Db 1441 ATGTCCCTGCTGGAATGTTTGTCCCTCTGTTTGAAACCATCGCTGCCCTGGAAGAT 1500
QY 1501 TACACCCACAGCACTGGAAGTGAAGTGGAGCTGGAGAGCAATCTTGCACTCTTCCTGGGG 1560
Db 1501 TACACCCACAGCACTGGAAGTGAAGTGGAGCTGGAGAGCAATCTTGCACTCTTCCTGGGG 1560
QY 1561 AACCTTAACAATTTCTTGGCCCTGATGGAATGATCGTCAACTCAAGCTTCTTAATGA 1620
Db 1561 AACCTTAACAATTTCTTGGCCCTGATGGAATGATCGTCAACTCAAGCTTCTTAATGA 1620

QY 1621 GAGCAATTAAGAACATCACTACATGACCTCTGTTTAACTATTACAATCTTCCTGGTTGG 1680
Db 1621 GAGCAATTAAGAACATCACTACATGACCTCTGTTTAACTATTACAATCTTCCTGGTTGG 1680
QY 1681 AACGAGATGTCCTCCCAACACCCCTGCACCTGCAAGATGTGCCGGGGTTCTTGCTGG 1740
Db 1681 AACGAGATGTCCTCCCAACACCCCTGCACCTGCAAGATGTGCCGGGGTTCTTGCTGG 1740
QY 1741 GAGCACTGTGGGCAATTGAATTCATGAGGCTGACGGTGTCTGACATGCTGGTAAAGTAC 1800
Db 1741 GAGCACTGTGGGCAATTGAATTCATGAGGCTGACGGTGTCTGACATGCTGGTAAAGTAC 1800
QY 1801 ATCAACATCCTGCTGGGGGACTTCACAGGACTTGTTTGTGGCGTTCAATGAACACTACG 1860
Db 1801 ATCAACATCCTGCTGGGGGACTTCACAGGACTTGTTTGTGGCGTTCAATGAACACTACG 1860
QY 1861 TGGTCTGGGACCTTGAAGCCTGGATTTCTTCATATGCTGAGTTGATATTAAGTGAAT 1920
Db 1861 TGGTCTGGGACCTTGAAGCCTGGATTTCTTCATATGCTGAGTTGATATTAAGTGAAT 1920
QY 1921 GTGCTGGGTTTGAATCTTCAACAAGAAATGATCTGGAATGGCTCTTCATGCTCCAGGC 1980
Db 1921 GTGCTGGGTTTGAATCTTCAACAAGAAATGATCTGGAATGGCTCTTCATGCTCCAGGC 1980
QY 1981 CTGGTGGGCAATTAATGTGCTGCGCCTGCTGACCTCCATGATCCAGATGCTGGGCGGTG 2040
Db 1981 CTGGTGGGCAATTAATGTGCTGCGCCTGCTGACCTCCATGATCCAGATGCTGGGCGGTG 2040
QY 2041 ATGAGAGCAAGTAAACCCCATGAAGCGTGTCAAAGCCTCCGATCCAAACAATCTTAC 2100
Db 2041 ATGAGAGCAAGTAAACCCCATGAAGCGTGTCAAAGCCTCCGATCCAAACAATCTTAC 2100
QY 2101 ATGGGCTCCTGCTGCTGTGTGCTCTTCCTCAAGCCTCCTGCGGATGGCTACACCATATG 2160
Db 2101 ATGGGCTCCTGCTGCTGTGTGCTCTTCCTCAAGCCTCCTGCGGATGGCTACACCATATG 2160
QY 2161 TCCCTCCACCTCCTTTGACTGCGGGCCGTTCAGTGGGAAAAACAAGATGACATGTC 2220
Db 2161 TCCCTCCACCTCCTTTGACTGCGGGCCGTTCAGTGGGAAAAACAAGATGACATGTC 2220
QY 2221 CTCGAGAGCAATGAAACGAATTCGCAACCTCTCGGCAAGATCTTGTGCTTCCTC 2280
Db 2221 CTCGAGAGCAATGAAACGAATTCGCAACCTCTCGGCAAGATCTTGTGCTTCCTC 2280
QY 2281 GCCAATCAGGCTGATCATCCAGCAATGCTGATGTTCTTGGCAATTAACACTG 2340
Db 2281 GCCAATCAGGCTGATCATCCAGCAATGCTGATGTTCTTGGCAATTAACACTG 2340
QY 2341 AACTCACTTCCAAAAGCTTTCGAGACTAATGCCAGCTGAGGAAGAAATCCAAATG 2400
Db 2341 AACTCACTTCCAAAAGCTTTCGAGACTAATGCCAGCTGAGGAAGAAATCCAAATG 2400
QY 2401 CTCGCTGAGTGTGAGAGAGTCAAAATCTGTAAAGGCAAGGCCAGCAAGTCA 2460
Db 2401 CTCGCTGAGTGTGAGAGAGTCAAAATCTGTAAAGGCAAGGCCAGCAAGTCA 2460

| | | | |
|----|------|--|------|
| QY | 2461 | GAGGACACACTTAAAGCAGCTCCAAATGCAACCACTCAACTCAGCAAGAGAG | 2520 |
| Db | 2461 | GAGGACACACTTAAAGCAGCTCCAAATGCAACCACTCAACTCAGCAAGAGAG | 2520 |
| QY | 2521 | ACCACTCCTCCCTGCGCCAGCAAAAGCAGGCAATGGACAAAGAGGCGCCCTGG | 2580 |
| Db | 2521 | ACCACTCCTCCCTGCGCCAGCAAAAGCAGGCAATGGACAAAGAGGCGCCCTGG | 2580 |
| QY | 2581 | ACCTCAATTCTGCCAGCAGCACTGCTGCTGCAACCTTCTATATCTCG | 2640 |
| Db | 2581 | ACCTCAATTCTGCCAGCAGCACTGCTGCTGCAACCTTCTATATCTCG | 2640 |
| QY | 2641 | CCCCCTGGAATCGGACAGATTCTGGCAGCGCCCATCTCAGACTCATCCGTGAAGTCA | 2700 |
| Db | 2641 | CCCCCTGGAATCGGACAGATTCTGGCAGCGCCCATCTCAGACTCATCCGTGAAGTCA | 2700 |
| QY | 2701 | GGCTCTGGAAAGATGCTCAGAGACCTCCCACTGAGGCTAGGACTCGAGGAGACCTCG | 2760 |
| Db | 2701 | GGCTCTGGAAAGATGCTCAGAGACCTCCCACTGAGGCTAGGACTCGAGGAGACCTCG | 2760 |
| QY | 2761 | ACCTTAGGGCTGATCCCTCAGTAACCCAGTTTCACACATACCAACAGTTCTCTCC | 2820 |
| Db | 2761 | ACCTTAGGGCTGATCCCTCAGTAACCCAGTTTCACACATACCAACAGTTCTCTCC | 2820 |
| QY | 2821 | CTCTTCTCTCAGATACATGCTCTGCTCTCTCTTGAATGCATGACTTTGATCTCT | 2880 |
| Db | 2821 | CTCTTCTCTCAGATACATGCTCTGCTCTCTCTTGAATGCATGACTTTGATCTCT | 2880 |
| QY | 2881 | TCAGGCGCTTGTCACTACCGAGAGAGAGAGATGGGCTTCACCTGCTCTTAAAGAG | 2940 |
| Db | 2881 | TCAGGCGCTTGTCACTACCGAGAGAGAGAGATGGGCTTCACCTGCTCTTAAAGAG | 2940 |
| QY | 2941 | CTGAGCCATCTCTGCACTAACTGCCCTCCAAATATCTTGGTTGAGACGCTTGAACC | 3000 |
| Db | 2941 | CTGAGCCATCTCTGCACTAACTGCCCTCCAAATATCTTGGTTGAGACGCTTGAACC | 3000 |
| QY | 3001 | CCAGCTTCAAGTGGTCCAGCTTGGCTCCCAATTTTCGAGTTGGGGAAGGCGCATGACC | 3060 |
| Db | 3001 | CCAGCTTCAAGTGGTCCAGCTTGGCTCCCAATTTTCGAGTTGGGGAAGGCGCATGACC | 3060 |
| QY | 3061 | ACCTCGTAGATTTTTCATGGATACAGTTTAGAGACAGGGGTTCTGCAAGTTCCT | 3120 |
| Db | 3061 | ACCTCGTAGATTTTTCATGGATACAGTTTAGAGACAGGGGTTCTGCAAGTTCCT | 3120 |
| QY | 3121 | AACGAGAGAGGGGATGAGAAAGGCTTACATTTCTCAATCAGAGAG | 3169 |
| Db | 3121 | AACGAGAGAGGGGATGAGAAAGGCTTACATTTCTCAATCAGAGAG | 3169 |

Search completed: November 30, 2005, 09:34:05
Job time : 15427 secs

OM nucleic - nucleic search, using sw model

Run on: November 30, 2005, 01:28:55 ; Search time 1704 Seconds

(without alignments)
12394.607 Million cell updates/sec

Title: US-10-792-307-3

Perfect score: 3169
Sequence: 1 gcagtgctgcgcacacagag.....attccatcatcagagagag 3169

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|------------|--------------------|
| 1 | 3074 | 97.0 | 3121 | 8 ACC69614 | ACC69614 Human tra |
| 2 | 2284.6 | 72.4 | 5027 | 5 AA92296 | AA92296 DNA encod |
| 3 | 1957.6 | 61.8 | 3216 | 8 ACC69616 | ACC69616 Mouse tra |
| 4 | 816.8 | 25.8 | 2895 | 8 ACC69615 | ACC69615 Mouse tra |

| | | | | | | |
|----|-------|------|------|----|----------|---------------------|
| 5 | 814.2 | 25.7 | 4333 | 8 | ACC69613 | Acc69613 Human tta |
| 6 | 591.8 | 18.7 | 2560 | 11 | ADM01657 | Adm01657 Human cDN |
| 7 | 463.4 | 14.6 | 2591 | 6 | ABV75613 | Abv75613 Human rlb |
| 8 | 437.6 | 13.8 | 3357 | 13 | ADU01837 | Adu01837 Novel hum |
| 9 | 356.4 | 11.2 | 3897 | 13 | ADU01668 | Adu01668 Novel hum |
| 10 | 308.6 | 9.7 | 3566 | 13 | ADU07531 | Adu07531 Full Leng |
| 11 | 193 | 6.1 | 5929 | 4 | ABL05865 | AbL05865 Drosophill |
| 12 | 104.6 | 3.3 | 1177 | 4 | AA546115 | Aa546115 Human DNA |
| 13 | 104.6 | 3.3 | 1177 | 6 | AAF92122 | AaF92122 Human PRO |
| 14 | 104.6 | 3.3 | 1177 | 6 | ABK33641 | AbK33641 cDNA, enco |
| 15 | 104.6 | 3.3 | 1177 | 6 | AB574442 | Ab574442 Human cDN |
| 16 | 104.6 | 3.3 | 1177 | 6 | ABL88207 | AbL88207 Human PRO |
| 17 | 104.6 | 3.3 | 1177 | 6 | ABL95696 | AbL95696 Human ang |
| 18 | 104.6 | 3.3 | 1177 | 7 | ADY31951 | Ady31951 Novel hum |
| 19 | 104.6 | 3.3 | 1177 | 8 | ACA89565 | AcA89565 cDNA, enco |
| 20 | 104.6 | 3.3 | 1177 | 8 | ACA73575 | AcA73575 Human sec |
| 21 | 104.6 | 3.3 | 1177 | 8 | ACA05890 | AcA05890 Human sec |
| 22 | 104.6 | 3.3 | 1177 | 8 | ACA66724 | AcA66724 cDNA, enco |
| 23 | 104.6 | 3.3 | 1177 | 8 | ACA91228 | AcA91228 Novel hum |
| 24 | 104.6 | 3.3 | 1177 | 8 | ACD81605 | AcD81605 Human cDN |
| 25 | 104.6 | 3.3 | 1177 | 8 | ACF20299 | AcF20299 Human sec |
| 26 | 104.6 | 3.3 | 1177 | 8 | ACF19685 | AcF19685 Human sec |
| 27 | 104.6 | 3.3 | 1177 | 8 | ACD21973 | AcD21973 Human sec |
| 28 | 104.6 | 3.3 | 1177 | 8 | ACF13138 | AcF13138 Human sec |
| 29 | 104.6 | 3.3 | 1177 | 8 | ACD23241 | AcD23241 Human sec |
| 30 | 104.6 | 3.3 | 1177 | 8 | ACF00290 | AcF00290 Human sec |
| 31 | 104.6 | 3.3 | 1177 | 8 | ACA60427 | AcA60427 Novel hum |
| 32 | 104.6 | 3.3 | 1177 | 8 | ACA72347 | AcA72347 Novel hum |
| 33 | 104.6 | 3.3 | 1177 | 8 | ACD04871 | AcD04871 Novel hum |
| 34 | 104.6 | 3.3 | 1177 | 8 | ACD18332 | AcD18332 Human sec |
| 35 | 104.6 | 3.3 | 1177 | 8 | ACD08339 | AcD08339 Human sec |
| 36 | 104.6 | 3.3 | 1177 | 8 | ACA88773 | AcA88773 Novel hum |
| 37 | 104.6 | 3.3 | 1177 | 8 | ACA70215 | AcA70215 Human sec |
| 38 | 104.6 | 3.3 | 1177 | 8 | ACD12437 | AcD12437 Novel hum |
| 39 | 104.6 | 3.3 | 1177 | 8 | ACC74352 | AcC74352 Human sec |
| 40 | 104.6 | 3.3 | 1177 | 8 | ACD15980 | AcD15980 Human sec |
| 41 | 104.6 | 3.3 | 1177 | 8 | ACD23548 | AcD23548 Novel hum |
| 42 | 104.6 | 3.3 | 1177 | 8 | ACD18025 | AcD18025 Human sec |
| 43 | 104.6 | 3.3 | 1177 | 8 | ACC88312 | AcC88312 Human sec |
| 44 | 104.6 | 3.3 | 1177 | 8 | ACD21666 | AcD21666 Human sec |
| 45 | 104.6 | 3.3 | 1177 | 8 | ACD18733 | AcD18733 Human sec |

ALIGNMENTS

RESULT 1
ACC69614 standard; cDNA; 3121 BP.

XX AC ACC69614;
XX DT 18-JUL-2003 (first entry)
XX DE Human transductin-2 (TDC2) encoding cDNA SEQ ID NO:3.
XX KW Human; transductin-2; TDC2; hearing loss; auditory; gene therapy; gene;

KW 59.
XX Homo sapiens.
OS Key Location/Qualifiers
XX CDS 16..2688
FT /'cag' a
FT /product= "transductin-2"
XX
XX W02003025140-A2.
XX 27-MAR-2003.
XX 19-SEP-2002; 2002MO-US029614.
XX 19-SEP-2001; 2001US-0323275P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Grlfith AV, Kurlima K, Wilcox E, Friedman T;
XX WPI: 2003-371806/35.
XX P-PSDB; ABR43616.
XX
XX An isolated or purified nucleic acid molecule encoding transductin-1
XX (TDC1), TDC2, or its fragment, useful for prognosticating, treating or
XX monitoring hearing loss.
XX
XX Claim 9; Fig 2; 85pp; English.
XX
XX The present sequence encodes human transductin-2 (TDC2). The present
XX invention describes human and mouse TDC1 and TDC2. Also described: (1) a
XX method for detecting hearing loss or predisposition to hearing loss in an
XX animal; (2) a method for determining the level of nucleic acid comprising
XX wild-type TDC1 or TDC2 gene and/or mutant TDC1 or TDC2 gene in a test
XX sample comprising a nucleic acid comprising the wild-type TDC1 or TDC2
XX gene and/or mutant TDC1 or TDC2 gene obtained from the animal; (3) a
XX method for detecting the level of wild-type TDC1 or TDC2, and/or mutant
XX TDC1 or TDC2 in a test sample comprising a protein comprising the wild-
XX type TDC1 or TDC2 gene and/or mutant TDC1 or TDC2 gene in a test sample
XX comprising a nucleic acid comprising the wild-type TDC1 or TDC2 gene
XX and/or mutant TDC1 or TDC2 gene obtained from the animal; (4) a method
XX for treating an animal prophylactically or therapeutically for hearing
XX loss due to a complete or partial loss of wild type TDC1 or TDC2; and (5)
XX a method for identifying one or more agents that interact with a TDC1
XX and/or TDC2 genes in a cell by administering one or more agents to the
XX cell comprising the genes and assaying the expression level of the genes
XX by the cell, where an increase or decrease in the expression level is
XX indicative of the interaction between the agents and the genes in the
XX cell. TDC1 and TDC2 have auditory activities and can be used in gene
XX therapy. The molecules, compositions and methods of the present invention
XX can be used for prognosticating, treating and monitoring hearing loss
XX
XX Sequence 3121 BP; 778 A; 823 C; 824 G; 696 T; 0 U; 0 Other;
XX
XX Query Match 97.0%; Score 3074; DB 8; Length 3121;
XX Best Local Similarity 100.0%; Pred. No. 0;

QY 1776 GGTGTGACATGCTGGTAACGTACATCCATCTCTGCTGGGGGACTTCCTACGGGCTTG 1835
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Db 1728 GGTGTGACATGCTGGTAACGTACATCCATCTCTGCTGGGGGACTTCCTACGGGCTTG 1787
1836 TTTTGTGGGGTTCATGAACCTACGCTGGTGGGACTTGGAGGCTGGATTCCTCATTA 1895
|||||
Db 1788 TTTTGTGGGGTTCATGAACCTACGCTGGTGGGACTTGGAGGCTGGATTCCTCATTA 1847
QY 1896 TGGTGAATTGATATTAGTGAAGATGTGCTGGGTTTGATCTTCAACCAAGGATGATCTG 1955
|||||
Db 1848 TGGTGAATTGATATTAGTGAAGATGTGCTGGGTTTGATCTTCAACCAAGGATGATCTG 1907
QY 1956 GATGGGCTCCTTCTATGCTCCAGGCTGGTGGGATTAATGTGCTGGGCTTGCTGACCTC 2015
|||||
Db 1908 GATGGGCTCCTTCTATGCTCCAGGCTGGTGGGATTAATGTGCTGGGCTTGCTGACCTC 1967
QY 2016 CATGTACTCCAGTGTGGGGGGTGGATGAGCAAGCAAGTACCCCATGAAAGGCTGTCAA 2075
|||||
Db 1968 CATGTACTCCAGTGTGGGGGGTGGATGAGCAAGCAAGTACCCCATGAAAGGCTGTCAA 2027
QY 2076 AGCCTCCCGATCCACAACTTCTACATGGGCTCTGCTGCTGGTGGTCTTCTCAAGCT 2135
|||||
Db 2028 AGCCTCCCGATCCACAACTTCTACATGGGCTCTGCTGCTGGTGGTCTTCTCAAGCT 2087
QY 2136 CCTGCCGGTGGCTACACATCATGTCCCTCCACCCCTCTTTGACTGGGGCCGTTCAAG 2195
|||||
Db 2088 CCTGCCGGTGGCTACACATCATGTCCCTCCACCCCTCTTTGACTGGGGCCGTTCAAG 2147
QY 2196 TGGGAAAAACAGATGTACGATGCTCTCCAAAGAGACATTTGAAAAGATTTCCCAACT 2255
|||||
Db 2148 TGGGAAAAACAGATGTACGATGCTCTCCAAAGAGACATTTGAAAAGATTTCCCAACT 2207
QY 2256 CCTGGGGAGATCTTTGCTTCTCTCCCAATCCAGGCTGATCATCCAGCCATCTGCT 2315
|||||
Db 2208 CCTGGGGAGATCTTTGCTTCTCTCCCAATCCAGGCTGATCATCCAGCCATCTGCT 2267
QY 2316 GATGTCTTGGCCATTACTACTGAACTCACTTTCCAAAAGCCCTTCCCAGCTAATGC 2375
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Db 2268 GATGTCTTGGCCATTACTACTGAACTCACTTTCCAAAAGCCCTTCCCAGCTAATGC 2327
QY 2376 CCAAGTGAAGAGAAAAATCCAAAGTCCGTAAGTTGAGAAAGTCACAAAATCTGTAA 2435
|||||
Db 2328 CCAAGTGAAGAGAAAAATCCAAAGTCCGTAAGTTGAGAAAGTCACAAAATCTGTAA 2387
QY 2436 AGGCAAAAGCCAAGCCAGAGATTCAAGAGACAACCTTAAAGCAAGCTCCAAAAATGCCA 2495
|||||
Db 2388 AGGCAAAAGCCAAGCCAGAGATTCAAGAGACAACCTTAAAGCAAGCTCCAAAAATGCCA 2447
QY 2496 CCAAGTCCAACTCACAAGAGAAAGACAACCTCCCTCTGCCAGCCAAAGCCAGGCAT 2555
|||||
Db 2448 CCAAGTCCAACTCACAAGAGAAAGACAACCTCCCTCTGCCAGCCAAAGCCAGGCAT 2507
QY 2556 GGACAAAGAGGGCCAGGGCCCTGGAGCTCCAAATTTGCTGACAGACGACCACTGCCTGC 2615
|||||
Db 2508 GGACAAAGAGGGCCAGGGCCCTGGAGCTCCAAATTTGCTGACAGACGACCACTGCCTGC 2567
QY 2616 CTCTGGAACCTTCTCTATATCTGGGCCCTGGAATGGACCAAGATTCTGGCAAGGCC 2675

Db 2568 CTCTGGAACCTTCTCTATATCTGGGCCCTTGGAAATCCGAACCAAGATTCTGGCCAGCCCC 2627
|||||
QY 2676 ATCTCAGACTCATCCGTGAGAGGTCAAGCTCTGGAAGAGTGTCAAGACCTCCCCACTG 2735
|||||
Db 2628 ATCTCAGACTCATCCGTGAGAGGTCAAGCTCTGGAAGAGTGTCAAGACCTCCCCACTG 2687
QY 2736 ACAGCTAGACTCCAGGAGACCTCGAACCTAGGGCTGATCCTCAAGTACCCAGTTTCA 2795
|||||
Db 2688 ACAGCTAGACTCCAGGAGACCTCGAACCTAGGGCTGATCCTCAAGTACCCAGTTTCA 2747
QY 2796 AATTAACCAACCAAGATTCTCTCCCTCTTCTCTCAATATAGTCTGTCTCTCTC 2855
|||||
Db 2748 AATTAACCAACCAAGATTCTCTCCCTCTTCTCTCAATATAGTCTGTCTCTCTC 2807
QY 2856 TTGGATGATGAATTTGATTCCTCAAGCCCTGTCAAGTACCGAAGAGAAAGCAG 2915
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Db 2808 TTGGATGATGAATTTGATTCCTCAAGCCCTGTCAAGTACCGAAGAGAAAGCAG 2867
QY 2916 TTGGCTTCACTGTCTCTTTAGGGAAGTGAAGCAATCTGTGACTAACTGGCCTCCAAAT 2975
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Db 2868 TTGGCTTCACTGTCTCTTTAGGGAAGTGAAGCAATCTGTGACTAACTGGCCTCCAAAT 2927
QY 2976 ATCTTGGTCAAGACGCTCTGAACCCCAAGCTCAAGTGTGCAAGCTTGCCTCCCAATT 3035
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Db 2928 ATCTTGGTCAAGACGCTCTGAACCCCAAGCTCAAGTGTGCAAGCTTGCCTCCCAATT 2987
QY 3036 TGGGAGTTGGGGAAGGACATGACCACTCGTAACTTTTTCATGGGATATACGTTAG 3095
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Db 2988 TGGGAGTTGGGGAAGGACATGACCACTCGTAACTTTTTCATGGGATATACGTTAG 3047
QY 3096 GACAAGGATTCTGCCAGCTTCCCTAACCAAGAGGGGATGGAAAGGCTTACATTCT 3155
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Db 3048 GACAAGGATTCTGCCAGCTTCCCTAACCAAGAGGGGATGGAAAGGCTTACATTCT 3107
QY 3156 CATTCAGAGGAAG 3169
|||||
Db 3108 CATTCAGAGGAAG 3121

RESULT 2
AAS92296
ID AAS92296 standard; cDNA; 5027 BP.
AC AAS92296;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #28100.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX W0200175067-A2.
XX

Db 1005 AGATACAAATTTCAAGCTTACTCAGTGGCTCTGGAGGCTCAGAAAATCTGCTTCAA 1064
QY 931 -----GTCTTTGGGATTTTGAAGGCTATATCAAGTACTGCACTCTTCTA 977
Db 1065 CCTTACTTATGTGGCTGTTCGAAAGGTTCAAGGCTATATCAAGTACTGCACTCTTCTA 1124
QY 978 TGGCTACTACACAAACAAGAGCAATCGGGTGGCTGAAGTACCGGGTGGCTATGGCTTA 1037
Db 1125 TGGTACTACACAAACAAGAGCAATCGGGTGGCTGAAGTACCGGGTGGCTATGGCTTA 1184
QY 1038 CTTTATGGTGGGGGTCAAGCTGTGGGCTACAGCTGATATGTGATTCATTCGATGGC 1097
Db 1185 CTTTATGGTGGGGGTCAAGCTGTGGGCTACAGCTGATATGTGATTCATTCGATGGC 1244
QY 1098 CAGCAATACCAAGGAAGACAGGGCGAAGGGAGATGCAACTTCATTCAGCTCAA 1157
Db 1245 CAGCAATACCAAGGAAGACAGGGCGAAGGGAGATGCAACTTCATTCAGCTCAA 1304
QY 1158 GATGTTCAACAAGCTGGGACTACCTGATCGGGAATTCAGAGACAGCTGATACAAATATGC 1217
Db 1305 GATGTTCAACAAGCTGGGACTACCTGATCGGGAATTCAGAGACAGCTGATACAAATATGC 1364
QY 1218 ATCCATCAACAAGCTTCAAGGAATCAATAGTGSATGAAAGAGAGTAAACAAAGAG 1277
Db 1365 ATCCATCAACAAGCTTCAAGGAATCAATAGTGSATGAAAGAGAGTAAACAAAGAG 1424
QY 1278 AATATCCATCTGACAGAGATTTCTTGGTGTCTGGCCAACTTCTCATGCTGTGTT 1337
Db 1425 AATATCCATCTGACAGAGATTTCTTGGTGTCTGGCCAACTTCTCATGCTGTGTT 1484
QY 1338 GTGTGAAAGTGGGTACCTCATTTACTTTGTGTTAAAGCACTCAGCAATTCGCAAAAT 1397
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QY 1398 GGAGATGTCAAGCTGATGAAAGGATGAGGTAGAGATCGTATGCCGTGTGGAT 1457
Db 1545 GGAGATGTCAAGCTGATGAAAGGATGAGGTAGAGATCGTATGCCGTGTGGAT 1604
QY 1458 GTTTTGTCCCCCTCTGTTTGAAACCATGCTGCCCTGAGAAATTACCAACCAACGCACTGG 1517
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QY 1518 ACTGAAGTGGAGCTGGAGCGCATCTTTGCACTCTTCTGGGAACTCTACACATTTCT 1577
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QY 1578 CTGGCCCTGATGATGACGTCCACCTCAAGCTTGGCTATGAGAGACAAATAAGAAAT 1637
Db 1725 CTGGCCCTGATGATGACGTCCACCTCAAGCTTGGCTATGAGAGACAAATAAGAAAT 1784
QY 1638 CACTCACTGGACTCTGTTTAACATTAACAACCTCTTGGTGGAGAGAGTGTCCCCG 1697
Db 1785 CACTCACTGGACTCTGTTTAACATTAACAACCTCTTGGTGGAGAGAGTGTCCCCG 1844
QY 1698 AACAACCCCTGACCTCGAGATGTGCCCGGGGTCTTCTGGAGAGACGTGTGGCAT 1757
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Db 1845 AACAACCCCTGACCTCGAGATGTGCCCGGGGTCTTCTGGAGAGACGCTGTGGCAT 1904
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QY 1818 GGACTTCCTACGGGCTGTTTTTGTGGGTTCAATGAATCTAGCTGGTGGAGCTTGA 1877
Db 1965 GGACTTCCTACGGGCTGTTTTTGTGGGTTCAATGAATCTAGCTGGTGGAGCTTGA 2024
QY 1878 GGGTGGATTTCTTCATATGCTGAGTTGATATATGAGAAATGTGGGGTTGATCTT 1937
Db 2025 GGGTGGATTTCTTCATATGCTGAGTTGATATATGAGAAATGTGGGGTTGATCTT 2084
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Db 2085 CAACCAAGGAATGATCTGATGGGCTCTTATGCTCAAGGCTGGTGGCATTAATGT 2144
QY 1998 GCTGGGCTGTGACCTGCATGTACTTCAGTGTCTGGGGGTGATGAGACAAAGTACC 2057
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Db 2205 CCATGAACGGGTGTTCAAAAGCTCCCAATCAAACTTCTAATGAGGCTCTGCTGCT 2264
QY 2118 GGTGCTCTTCTCAGGCTCCTGGCGGTGGCTACAACATCATGTCCCTCCACCTCCT 2177
Db 2265 GGTGCTCTTCTCAGGCTCCTGGCGGTGGCTACAACATCATGTCCCTCCACCTCCT 2324
QY 2178 TGACTGGGGCCGTTCAGTGGGAAAAACAGATGTACAGTGTCTTCAGAGACATTTGA 2237
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Db 2385 AAACGATTTCCCAACTTCTGGGCAAGATCTTGTCTTCTGSCCAATCCAGGCTGAT 2444
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Db 2685 CAGCCAAAGCAGGCATGGAAGAGAGGGCGAGGCGTGGAGCTCCAAATTTCTGCAAG 2744
|||||

[illegible]

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|-------------------|---------------------|
| c 1 | 96 | 3.0 | 7218 | 2 | US-08-232-463-14 | Sequence 14, Appl1 |
| 2 | 76.4 | 2.4 | 2001 | 3 | US-09-799-451-695 | Sequence 699, Appl1 |
| 3 | 51.6 | 1.6 | 7218 | 2 | US-08-232-463-14 | Sequence 14, Appl1 |
| 4 | 50 | 1.6 | 1926 | 3 | US-09-249-584-2 | Sequence 2, Appl1 |
| 5 | 50 | 1.6 | 1926 | 3 | US-09-410-399-3 | Sequence 3, Appl1 |
| 6 | 50 | 1.6 | 2580 | 3 | US-09-050-863-2 | Sequence 2, Appl1 |
| 7 | 50 | 1.6 | 2580 | 3 | US-09-359-081-2 | Sequence 2, Appl1 |
| 8 | 50 | 1.6 | 5452 | 2 | US-09-130-114-1 | Sequence 1, Appl1 |
| 9 | 50 | 1.6 | 8705 | 3 | US-09-647-344A-14 | Sequence 14, Appl1 |

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| 10 | 50 | 1.6 | 9600 | 3 | US-08-910-647-1 | Sequence 1, Appl1 |
| 11 | 50 | 1.6 | 9600 | 3 | US-09-620-925-1 | Sequence 1, Appl1 |
| 12 | 50 | 1.6 | 10596 | 2 | US-07-884-811-15 | Sequence 15, Appl1 |
| 13 | 50 | 1.6 | 10596 | 2 | US-07-885-971-15 | Sequence 15, Appl1 |
| 14 | 50 | 1.6 | 10596 | 2 | US-08-087-783A-15 | Sequence 15, Appl1 |
| 15 | 50 | 1.6 | 10596 | 2 | US-08-194-088B-15 | Sequence 15, Appl1 |
| 16 | 50 | 1.6 | 10596 | 2 | US-08-194-087-15 | Sequence 15, Appl1 |
| 17 | 50 | 1.6 | 10596 | 6 | PCT-US93-04648-15 | Sequence 48, Appl1 |
| 18 | 50 | 1.6 | 16080 | 3 | US-09-724-566A-48 | Sequence 2, Appl1 |
| 19 | 50 | 1.6 | 16080 | 3 | US-09-471-669A-48 | Sequence 208, App |
| 20 | 48 | 1.5 | 16442 | 3 | US-08-781-891-208 | Sequence 208, App |
| 21 | 48 | 1.5 | 16442 | 3 | US-09-618-166-208 | Sequence 208, App |
| 22 | 48 | 1.5 | 53577 | 3 | US-08-658-136-2 | Sequence 1, Appl1 |
| 23 | 48 | 1.5 | 53577 | 3 | US-08-658-136-1 | Sequence 1, Appl1 |
| 24 | 48 | 1.5 | 53577 | 3 | US-08-460-215A-1 | Sequence 1200, Ap |
| 25 | 47.8 | 1.5 | 507 | 3 | US-09-489-039A-1200 | Sequence 1064, Ap |
| 26 | 47.8 | 1.5 | 516 | 3 | US-09-489-039A-1064 | Sequence 1065, Ap |
| 27 | 47.8 | 1.5 | 537 | 3 | US-09-489-039A-1065 | Sequence 1130, Ap |
| 28 | 47.8 | 1.5 | 549 | 3 | US-09-489-039A-1130 | Sequence 1011, Ap |
| 29 | 47.8 | 1.5 | 558 | 3 | US-09-489-039A-1011 | Sequence 4, Appl1 |
| 30 | 47.8 | 1.5 | 609 | 3 | US-09-489-039A-1177 | Sequence 2, Appl1 |
| 31 | 46.8 | 1.5 | 1926 | 3 | US-09-249-585A-4 | Sequence 1886, A |
| 32 | 46.8 | 1.5 | 1931 | 2 | US-09-130-114-2 | Sequence 1666, A |
| 33 | 46.6 | 1.5 | 6644 | 3 | US-08-875-435B-5 | Sequence 1, Appl1 |
| 34 | 46.2 | 1.5 | 39489 | 3 | US-09-949-016-13886 | Sequence 20, Appl1 |
| 35 | 45.8 | 1.4 | 2093 | 2 | US-10-104-047-1666 | Sequence 20, Appl1 |
| 36 | 44.8 | 1.4 | 3489 | 2 | US-08-728-323A-1 | Sequence 1, Appl1 |
| 37 | 44.8 | 1.4 | 3489 | 3 | US-09-298-568-1 | Sequence 1, Appl1 |
| 38 | 44.8 | 1.4 | 3489 | 3 | US-09-410-399-1 | Sequence 1, Appl1 |
| 39 | 44.8 | 1.4 | 3489 | 3 | US-09-894-273-1 | Sequence 20, Appl1 |
| 40 | 44.8 | 1.4 | 32207 | 2 | US-08-770-379-20 | Sequence 20, Appl1 |
| 41 | 44.8 | 1.4 | 32207 | 3 | US-08-757-669A-20 | Sequence 20, Appl1 |
| 42 | 44.8 | 1.4 | 32207 | 3 | US-09-230-371A-20 | Sequence 10, Appl1 |
| 43 | 44 | 1.4 | 1408 | 2 | US-08-222-124-10 | Sequence 9, Appl1 |
| 44 | 44 | 1.4 | 1408 | 2 | US-08-842-657A-10 | Sequence 9, Appl1 |
| 45 | 44 | 1.4 | 1414 | 2 | US-08-222-124-9 | |

Search completed: November 30, 2005, 12:49:43
Job time : 572 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 30, 2005, 06:00:20 ; Search time 2220 Seconds
(without alignments)
11804.351 Million cell updates/sec

Title: US-10-792-307-3
Perfect score: 3169
Sequence: 1 gcagtcgtcgcacagag.....atttcacatccagagag 3169

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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| 2: | /cgn2_6/ptcdatc/1/pubpna/US08_PUBCOMB.seq:* |
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| 10: | /cgn2_6/ptcdatc/1/pubpna/US11_PUBCOMB.seq:* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 3169 | 100.0 | 3169 | 9 | US-10-792-307-3 |
| 2 | 3074 | 97.0 | 3121 | 8 | US-10-487-887-3 |
| 3 | 2294.6 | 72.4 | 5027 | 9 | US-10-450-763-28100 |
| 4 | 2293 | 72.4 | 4895 | 6 | US-10-115-831-134 |
| 5 | 1957.6 | 61.8 | 3216 | 8 | US-10-487-887-7 |
| 6 | 1957.6 | 61.8 | 3216 | 9 | US-10-792-307-7 |
| 7 | 816.8 | 25.8 | 2895 | 8 | US-10-487-887-5 |
| 8 | 816.8 | 25.8 | 2895 | 9 | US-10-792-307-5 |

9 814.2 25.7 4333 8 US-10-487-887-1 Sequence 1, Appli
10 814.2 25.7 4333 9 US-10-792-307-1 Sequence 1, Appli
11 591.8 18.7 2560 6 US-10-108-260A-342 Sequence 342, App
12 193 6.1 5929 10 US-11-097-143-6038 Sequence 6038, Ap
13 154.4 4.9 1060 5 US-10-027-632-122322 Sequence 122322,
14 154.4 4.9 1060 6 US-10-027-632-122322 Sequence 122322,
15 104.6 3.3 1177 5 US-10-006-867-129 Sequence 129, App
16 104.6 3.3 1177 5 US-10-052-586-381 Sequence 381, App
17 104.6 3.3 1177 5 US-10-063-547-129 Sequence 129, App
18 104.6 3.3 1177 5 US-10-063-551-129 Sequence 129, App
19 104.6 3.3 1177 5 US-10-174-590-381 Sequence 381, App
20 104.6 3.3 1177 5 US-10-176-758-381 Sequence 381, App
21 104.6 3.3 1177 5 US-10-175-737-381 Sequence 381, App
22 104.6 3.3 1177 5 US-10-063-616-129 Sequence 129, App
23 104.6 3.3 1177 5 US-10-174-581-381 Sequence 381, App
24 104.6 3.3 1177 5 US-10-176-483-381 Sequence 381, App
25 104.6 3.3 1177 5 US-10-176-749-381 Sequence 381, App
26 104.6 3.3 1177 5 US-10-176-914-381 Sequence 381, App
27 104.6 3.3 1177 5 US-10-176-915-381 Sequence 381, App
28 104.6 3.3 1177 5 US-10-063-569-129 Sequence 129, App
29 104.6 3.3 1177 5 US-10-063-513-129 Sequence 129, App
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32 104.6 3.3 1177 5 US-10-173-738-381 Sequence 381, App
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34 104.6 3.3 1177 5 US-10-176-482-381 Sequence 381, App
35 104.6 3.3 1177 5 US-10-176-757-381 Sequence 381, App
36 104.6 3.3 1177 5 US-10-176-913-381 Sequence 381, App
37 104.6 3.3 1177 5 US-10-180-557-381 Sequence 381, App
38 104.6 3.3 1177 5 US-10-180-557-381 Sequence 381, App
39 104.6 3.3 1177 5 US-10-063-502-129 Sequence 129, App
40 104.6 3.3 1177 5 US-10-173-700-381 Sequence 381, App
41 104.6 3.3 1177 5 US-10-174-572-381 Sequence 381, App
42 104.6 3.3 1177 5 US-10-174-579-381 Sequence 381, App
43 104.6 3.3 1177 5 US-10-174-582-381 Sequence 381, App
44 104.6 3.3 1177 5 US-10-174-588-381 Sequence 381, App
45 104.6 3.3 1177 5 US-10-174-588-381 Sequence 381, App

ALIGNMENTS

RESULT 1
US-10-792-307-3
; Sequence 3, Application US/10792307
; Publication No. US20050196759A1
; GENERAL INFORMATION:
; APPLICANT: Griffith, Andrew J.
; APPLICANT: Kurihara, Kiyoko
; APPLICANT: Wilcox, Edward
; APPLICANT: Friedman, Thomas
; TITLE OF INVENTION: TRANSDUCTIN-1 AND TRANSDUCTIN-2 AND APPLICATIONS TO
HEREDITARY
; TITLE OF INVENTION: DEAFNESS
; FILE REFERENCE: 227540
; CURRENT APPLICATION NUMBER: US/10792,307
; CURRENT FILING DATE: 2004-03-03

; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patencin version 3.2
; SEQ ID NO 3
; LENGTH: 3169
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-792-307-3

Query Match 100.0%; Score 3169; DB 9; Length 3169;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 GCATGCTGCTGACCAATGACCAACCAAGGCTTGAAGAGAGCAAGCGGA 60

61 GTGAAGGGGGGTGAAGGGGCTCTCAACACACAGTGAACAGTGGGAGATTC 120
61 GTGAAGGGGGGTGAAGGGGCTCTCAACACACAGTGAACAGTGGGAGATTC 120

121 TCAACAAAGGGGCTCTCAACAGGAGACCCAGGAGGAGGAGCTCAGGAAAG 180
121 TCAACAAAGGGGCTCTCAACAGGAGACCCAGGAGGAGGAGCTCAGGAAAG 180

181 CAGAAAGAGCGCGCGGGGAGCCCAAGCCGAGGCTCTCCCGAGAGCAACAGG 240
181 CAGAAAGAGCGCGCGGGGAGCCCAAGCCGAGGCTCTCCCGAGAGCAACAGG 240

241 CCGAAGAGACACAGAAAGCTGGGGAGACAGAGAGCGGGGAGAGGAGAGCTGC 300
241 CCGAAGAGACACAGAAAGCTGGGGAGACAGAGAGCGGGGAGAGGAGAGCTGC 300

301 GAGGCGAGGAAAGCGCGAGCGAGGGGCTCTTCCAGAGCGGACAGCCCAAG 360
301 GAGGCGAGGAAAGCGCGAGCGAGGGGCTCTTCCAGAGCGGAGAGCCCAAG 360

361 AGGAGAAAGAGATTCGAGAGAGAGAGAGTCCAGAGCGGAGAGAAACCCAGGTC 420
361 AGGAGAAAGAGATTCGAGAGAGAGAGAGTCCAGAGCGGAGAGAAACCCAGGTC 420

421 TCCTGCTTGGCTCCAGTGCCTGCTGGTGGGAGTCCCTGTCCAGAGAGACTGGCC 480
421 TCCTGCTTGGCTCCAGTGCCTGCTGGTGGGAGTCCCTGTCCAGAGAGACTGGCC 480

481 ATCTGAGAGAGTGAAGAGAGAGAGAGTCAATGGCAAGTGGAGAGAGAGAGAG 540
481 ATCTGAGAGAGTGAAGAGAGAGAGAGTCAATGGCAAGTGGAGAGAGAGAGAG 540

541 CCGATGGCGAGAGAGTGAAGAGAGTCAAGGAGGCGGAGAGATTTGGAGAGATGA 600
541 CCGATGGCGAGAGAGTGAAGAGAGTCAAGGAGGCGGAGAGATTTGGAGAGATGA 600

601 GGTGCTTGGGAGAGAGAGAGAGAGTATGGCTCAAGAGTGTGATGGGCAAG 660
601 GGTGCTTGGGAGAGAGAGAGAGAGTATGGCTCAAGAGTGTGATGGGCAAG 660

661 AATGGGTCAAATTTAAGAGAGCTTGAATATTCAGAGTCAATGATCCCTGGGAA 720
661 AATGGGTCAAATTTAAGAGAGCTTGAATATTCAGAGTCAATGATCCCTGGGAA 720

Db ||||| 661 AAATGGGCAAAATTTAAGAGACTTGTATATTTCAAGACTCAATGTATCCCGGGAA 720
QY 721 ATGAAGATCAAGGACATTGAAGTCACTTGGTCTTCAAGTGGACGTATTTCATCTTT 780
Db ||||| 721 ATGAAGATCAAGGACATTGAAGTCACTTGGTCTTCAAGTGGACGTATTTCATCTTT 780
QY 781 CTCGAGTGAATGATGAAGTTAACCTTGTCTTTTGGCTTAATATTGGCTAGTCAATA 840
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Db |||||

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Db 1561 AACCTACACATTTCTCTTGGGCTGATGGAATGACGTCCACGTCAAGCTTGTAAATGA 1620
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Db 1621 GAGCAATTAAGAACATCACTCACTGGAATCTGTGTTAACTATTACAACTCTTGGTTGG 1680
QY 1681 AACGAGATGTCCGCCACCAACCTGACACCTGCAAGATGTGCCCGGGGTCTTGGCTGG 1740
Db 1681 AACGAGATGTCCGCCACCAACCTGACACCTGCAAGATGTGCCCGGGGTCTTGGCTGG 1740
QY 1741 GAGCACTGTGGGATTTGAATTCATGAGGCTGACGATGTCTGACATGCTGGTAAGTAC 1800
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Db 1801 ATCAACATCCTGCTGGGGGACTTCCATACGGGCTTGTGTTGGGTTCAAGACTATGC 1860
QY 1861 TGGTCTGGGACTTGAAGGCTGGAATTTCTCTCAATGCTGAGTTGATTAATAGTGAAT 1920
Db 1861 TGGTCTGGGACTTGAAGGCTGGAATTTCTCTCAATGCTGAGTTGATTAATAGTGAAT 1920
QY 1921 GTGCTGGGTTTGAATCTTCAACAAGAAATGATGGAATGGGCTCTTCTATGCTCCAGGC 1980
Db 1921 GTGCTGGGTTTGAATCTTCAACAAGAAATGATGGAATGGGCTCTTCTATGCTCCAGGC 1980
QY 1981 CTGGTGGGCAATTAATGTGCTGGGCTGCTGACCTCATGTACTTCAAGTGGTGGGCGGTG 2040
Db 1981 CTGGTGGGCAATTAATGTGCTGGGCTGCTGACCTCATGTACTTCAAGTGGTGGGCGGTG 2040
QY 2041 ATGAGAGCAAGTAAACCCATGAACGGTGTCAAAAGGCTCCGATCCAAACTTCTAC 2100
Db 2041 ATGAGAGCAAGTAAACCCATGAACGGTGTCAAAAGGCTCCGATCCAAACTTCTAC 2100
QY 2101 ATGGGCTCTGCTGCTGCTGCTCTTCTCAAGCTCTGCGGGTGGCTTACACCATCATG 2160
Db 2101 ATGGGCTCTGCTGCTGCTGCTCTTCTCAAGCTCTGCGGGTGGCTTACACCATCATG 2160
QY 2161 TCCCTCCACCTCTCTTGACTGCGGGCTTCAAGTGGGAAAAAGAAATGTACGATGTC 2220
Db 2161 TCCCTCCACCTCTCTTGACTGCGGGCTTCAAGTGGGAAAAAGAAATGTACGATGTC 2220
QY 2221 CTCGAGAGCAATTAAGAAATGTCGAAACCTTCTGGGCAAGATCTTGGCTTCTGTC 2280
Db 2221 CTCGAGAGCAATTAAGAAATGTCGAAACCTTCTGGGCAAGATCTTGGCTTCTGTC 2280
QY 2281 GCGAATTCAGGCTGATCATCCAGCAATCTGCTGATGTTCTTGGGCAATTTACTACGT 2340
Db 2281 GCGAATTCAGGCTGATCATCCAGCAATCTGCTGATGTTCTTGGGCAATTTACTACGT 2340
QY 2341 AACTCAGTTTCCAAAAGCTTCCGAGCTTAATGCCAGCTTGAAGAAAGAAATCCAAAGT 2400
Db 2341 AACTCAGTTTCCAAAAGCTTCCGAGCTTAATGCCAGCTTGAAGAAAGAAATCCAAAGT 2400

QY 2401 CTCGCTGAAGTGAAGAGTCACAATCTGTAAAAAGCAAGCCACAGCAGATTCA 2460
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Db 2401 CTCGCTGAAGTGAAGAGTCACAATCTGTAAAAAGCAAGCCACAGCAGATTCA 2460
2461 GAGGACACACTAAAAAGAGTCCAAAAATGCACCCAGCTCCAACTCACACAGAGAG 2520
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Db 2461 GAGGACACACTAAAAAGAGTCCAAAAATGCACCCAGCTCCAACTCACACAGAGAG 2520
QY 2521 ACCACTCTCCCTCTGCCAGCAAAACCCAGGCTATGGAAGAAAAGGCGGCGCTGG 2580
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Db 2521 ACCACTCTCCCTCTGCCAGCAAAACCCAGGCTATGGAAGAAAAGGCGGCGCTGG 2580
QY 2581 ACCTCCAACTTCTGCAGAGCAACAACCTGCTGCTGCAACACTTCTCTATCTCG 2640
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Db 2581 ACCTCCAACTTCTGCAGAGCAACAACCTGCTGCTGCAACACTTCTCTATCTCG 2640
QY 2641 CCCCCCTGGAAATCCGACCAATTTGGCCACGCCCCATCTCAGACTCATCCGTGAGGTCA 2700
|||||
Db 2641 CCCCCCTGGAAATCCGACCAATTTGGCCACGCCCCATCTCAGACTCATCCGTGAGGTCA 2700
QY 2701 GCCTCTGAAAAGAGTCTCAGAGACCTCCCACTGAGGCTAGACTCCAGGAGCCCTCG 2760
|||||
Db 2701 GCCTCTGAAAAGAGTCTCAGAGACCTCCCACTGAGGCTAGACTCCAGGAGCCCTCG 2760
QY 2761 ACCCTAGGGGCTGATCCCTCAAGTACCCCAATTTCAACATACCAACCAAGTTCTCTCC 2820
|||||
Db 2761 ACCCTAGGGGCTGATCCCTCAAGTACCCCAATTTCAACATACCAACCAAGTTCTCTCC 2820
QY 2821 CTCCTTCTCTCAGATACATGCTCTGCTCTCTTGGATGATGACTTATTCCT 2880
|||||
Db 2821 CTCCTTCTCTCAGATACATGCTCTGCTCTCTTGGATGATGACTTATTCCT 2880
QY 2881 TCAGGCCCTTGTCAAGTACCGAAGAGAGAGAGTGGCTTCACTGCTCTTGAAGAG 2940
|||||
Db 2881 TCAGGCCCTTGTCAAGTACCGAAGAGAGAGAGTGGCTTCACTGCTCTTGAAGAG 2940
QY 2941 CTGGAGCCATCTCTGACTAACTGCCCTCCCAATATCTTGGTTCAAGACGCTTGAAAC 3000
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Db 2941 CTGGAGCCATCTCTGACTAACTGCCCTCCCAATATCTTGGTTCAAGACGCTTGAAAC 3000
QY 3001 CCAGGCTCAAGTGGTGGAGCTTGGCTCCCAATTTTCGAGTTGGGGAAGGGCCATGACC 3060
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Db 3001 CCAGGCTCAAGTGGTGGAGCTTGGCTCCCAATTTTCGAGTTGGGGAAGGGCCATGACC 3060
QY 3061 ACCCTCGAAGCTTTTCCATGGGATACAGTTTAGACAACGGGTTTCTGCAAGCTCCCT 3120
|||||
Db 3061 ACCCTCGAAGCTTTTCCATGGGATACAGTTTAGACAACGGGTTTCTGCAAGCTCCCT 3120
QY 3121 AACCAAGAGGGGAGTGAAGAGGCTTCTCAATCCAGAGAG 3169
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Db 3121 AACCAAGAGGGGAGTGAAGAGGCTTCTCAATCCAGAGAG 3169

RESULT 2.
US-10-487-887-3
; Sequence 3, Application US/10487887

/ Publication No. US20040249139A1
/ GENERAL INFORMATION:
/ APPLICANT: Griffith, Andrew J
/ APPLICANT: Kurime, Kiyoto
/ APPLICANT: Wilcox, Edward
/ APPLICANT: Friedman, Thomas
/ TITLE OF INVENTION: TRANSDUCTIN-1 AND TRANSDUCTIN-2 AND APPLICATIONS TO
HEREDITARY
/ TITLE OF INVENTION: DEAFNESS
/ FILE REFERENCE: 226544
/ CURRENT APPLICATION NUMBER: US/10/487,887
/ CURRENT FILING DATE: 2004-02-26
/ PRIOR APPLICATION NUMBER: PCT/US02/29614
/ PRIOR FILING DATE: 2002-09-19
/ PRIOR APPLICATION NUMBER: 60/323,275
/ PRIOR FILING DATE: 2001-09-19
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 3
/ LENGTH: 3121
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-487-887-3

Query Match 97.0%; Score 3074; DB 8; Length 3121;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3074; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 AGGTGACAGGCTGGGAGAGAGTCTCAAGCAAGGGGCTCTCAAGCCGAGGGAGCCCC 155
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Db 48 AGGTGACAGGCTGGGAGAGAGTCTCAAGCAAGGGGCTCTCAAGCCGAGGGAGCCCC 107
156 AGGAGGCGGGAGGCTCAGCGAAGCAGAAAGAGAGCGCCGCGGAGCAAGCCAGCCGG 215
|||||
Db 108 AGGAGGCGGGAGGCTCAGCGAAGCAGAAAGAGAGCGCCGCGGAGCAAGCCAGCCGG 167
QY 216 GTCTCCCCGAGAGAAAGCAAGGGCGCAGAGACACAGAGAGAGACTGGGGAGCGAGA 275
|||||
Db 168 GTCTCCCCGAGAGAAAGCAAGGGCGCAGAGACACAGAGAGAGACTGGGGAGCGAGA 227
276 GCGGGGCGAGGAGAGAGCTCCAGGGCAGAGAAAGGCGGAGAGAGGGGCTCTT 335
|||||
Db 228 GCGGGGCGAGGAGAGAGCTCCAGGGCAGAGAAAGGCGGAGAGAGGGGCTCTT 287
QY 336 CCAAGAGCGGACAGAGCCCAAGAGGAGAAAGGAGATTCCAGAGAGAGAGAGATC 395
|||||
Db 288 CCAAGAGCGGACAGAGCCCAAGAGGAGAAAGGAGATTCCAGAGAGAGAGAGATC 347
QY 396 GAGGGGCAAGAAAGAAAGCAAGTCACTCTCTGGCTCCAGTGCTCTGGTGGGAGTC 455
|||||
Db 348 GAGGGGCAAGAAAGAAAGCAAGTCACTCTCTGGCTCCAGTGCTCTGGTGGGAGTC 407
QY 456 CCGTCCGAGAGAGAGTGGCCAGATCTGAGAGAGTGGAGAGAAAGAAAGAGCTCAT 515
|||||
Db 408 CCGTCCGAGAGAGAGTGGCCAGATCTGAGAGAGTGGAGAGAGAAAGAAAGAGCTCAT 467
QY 516 TCCACCAATGCCAGCAAGCCCTGGCCCATGGCGAAGAGGCTGACAGAGCTCAGGAGGCG 575

| | | | | |
|----|--|------|---|------|
| Db | | 1468 | TGCCACATCGGAGCAAGCCCTGGCCCATGGCCAGAAAGCTGACAGAGCTCAGGGAGGC | 527 |
| QY | | 576 | CCAGGAATTTGTGGAGAAATGTGAAGTGCCTTGGGAAAGGGGAAAGGCAACAACTATA | 635 |
| Db | | 528 | CCAGGAATTTGTGGAGAAATGTGAAGTGCCTTGGGAAAGGGGAAAGGCAACAACTATA | 587 |
| QY | | 636 | TGCCTACAAGATGCTGATGGCCAGAAATGGGTCAAAATTTAAGAGACTTTGATATTT | 695 |
| Db | | 588 | TGCCTACAAGATGCTGATGGCCAGAAATGGGTCAAAATTTAAGAGACTTTGATATTT | 647 |
| QY | | 696 | CAAGACTCAATGATCCCTGGGAAATGAAGATCAAGACATGGAAGTCACTTTGGTTC | 755 |
| Db | | 648 | CAAGACTCAATGATCCCTGGGAAATGAAGATCAAGACATGGAAGTCACTTTGGTTC | 707 |
| QY | | 756 | TTCACTGGCATGGTATTTCACTTTCTCCGATGGAATGATGGAATTAACCTTGTCTTTT | 815 |
| Db | | 708 | TTCACTGGCATGGTATTTCACTTTCTCCGATGGAATGATGGAATTAACCTTGTCTTTT | 767 |
| QY | | 816 | TGCCTTAATATTTGGTCTAGTCAATCCAGAGTACTGATGGGCATGGCCTATGGAG | 875 |
| Db | | 768 | TGCCTTAATATTTGGTCTAGTCAATCCAGAGTACTGATGGGCATGGCCTATGGAG | 827 |
| QY | | 876 | TATCCCAAGAAACAGTGCCTCGGGCTGAGGAAAGGCAATGGATTTTCTGTCT | 935 |
| Db | | 828 | TATCCCAAGAAACAGTGCCTCGGGCTGAGGAAAGGCAATGGATTTTCTGTCT | 887 |
| QY | | 936 | TTGGATTTTGAAGGCTATATCAAGTACTGCACTCTTCTATGGCTACTACAAACCA | 995 |
| Db | | 888 | TTGGATTTTGAAGGCTATATCAAGTACTGCACTCTTCTATGGCTACTACAAACCA | 947 |
| QY | | 996 | GAGGACATCGGGTGGCTGAGGTACCGGCTGCCTATGGCTTACTTATGGTGGGGTCAG | 1055 |
| Db | | 948 | GAGGACATCGGGTGGCTGAGGTACCGGCTGCCTATGGCTTACTTATGGTGGGGTCAG | 1007 |
| QY | | 1056 | CGTGTGGCTACAGCTGATTAATGTCAATCGATGAGTGCAGCAATACCAAGGAG | 1115 |
| Db | | 1008 | CGTGTGGCTACAGCTGATTAATGTCAATCGATGAGTGCAGCAATACCAAGGAG | 1067 |
| QY | | 1116 | CACAGGCGAAGGGAGAGTGCACAACTTCACATTCAGCTTCAGAGTGCACAGCTGGGA | 1175 |
| Db | | 1068 | CACAGGCGAAGGGAGAGTGCACAACTTCACATTCAGCTTCAGAGTGCACAGCTGGGA | 1127 |
| QY | | 1176 | CTACCTGATCGGGAATTCAGAGACAGCTGATTAACAAATATGCATCAACCAACGCTT | 1235 |
| Db | | 1128 | CTACCTGATCGGGAATTCAGAGACAGCTGATTAACAAATATGCATCAACCAACGCTT | 1187 |
| QY | | 1236 | CAAGGAATCAATAGTGAATGAACAAAGATACAAAGAAATATCCATCTGACAG | 1295 |
| Db | | 1188 | CAAGGAATCAATAGTGAATGAACAAAGATACAAAGAAATATCCATCTGACAG | 1247 |
| QY | | 1296 | ATTTCTTCTGTCTGTGGCAACTTTCTCATCTGCTGTGTTGTGTGAAGTGGGTACCT | 1355 |
| Db | | 1248 | ATTTCTTCTGTCTGTGGCAACTTTCTCATCTGCTGTGTTGTGTGAAGTGGGTACCT | 1307 |
| QY | | 1356 | CATTTACTTTTGTGTTAAAGCAATCTCAGCAATCTCCAAATGCAGAAATGTCAGCTGTA | 1415 |
| Db | | | | |
| Db | | 1308 | CATTTACTTTTGTGTTAAAGCAATCTCAGCAATCTCCAAATGCAGAAATGTCAGCTGTA | 1367 |
| QY | | 1416 | TGAAGGAATGAGGTAGAGATGTGATGTCCCTGCTTGGATGTTTTGTCCCTCTGTT | 1475 |
| Db | | 1368 | TGAAGGAATGAGGTAGAGATGTGATGTCCCTGCTTGGATGTTTTGTCCCTCTGTT | 1427 |
| QY | | 1476 | TGAAGCAATGGCTGCCCTGGAGAAATTACACCCACGCACTGGACTGAGTGGAGCTGGG | 1535 |
| Db | | 1428 | TGAAGCAATGGCTGCCCTGGAGAAATTACACCCACGCACTGGACTGAGTGGAGCTGGG | 1487 |
| QY | | 1536 | ACGCATCTTTGCACTTTCTTCTGGGGACCTCTACACATTTTCTCTTGGCCCTGATGATTA | 1595 |
| Db | | 1488 | ACGCATCTTTGCACTTTCTTCTGGGGACCTCTACACATTTTCTCTTGGCCCTGATGATTA | 1547 |
| QY | | 1596 | CGTCAACCTCAAGCTGCTTAATGAAGACATAAAGAACTCACTCACTGGAAGCTGTT | 1655 |
| Db | | 1548 | CGTCAACCTCAAGCTGCTTAATGAAGACATAAAGAACTCACTCACTGGAAGCTGTT | 1607 |
| QY | | 1656 | TAACTATTACAACCTTCTGTGTTGGACGAGTGTCCCGACACACCCCTGCACCCCTGC | 1715 |
| Db | | 1608 | TAACTATTACAACCTTCTGTGTTGGACGAGTGTCCCGACACACCCCTGCACCCCTGC | 1667 |
| QY | | 1716 | AGATGTCCCGGGGTTCTTGTGTGGAGACAGCTGTGGGCAATGAAATTCATGAGGCTGAC | 1775 |
| Db | | 1668 | AGATGTCCCGGGGTTCTTGTGTGGAGACAGCTGTGGGCAATGAAATTCATGAGGCTGAC | 1727 |
| QY | | 1776 | GGTGTCAACATGCTGTGTAACATACACATCTGCTGGGGGACCTTCTACGGGCTTG | 1835 |
| Db | | 1728 | GGTGTCAACATGCTGTGTAACATACACATCTGCTGGGGGACCTTCTACGGGCTTG | 1787 |
| QY | | 1836 | TTTTGTGCGGTTCAATGAACACTGCTGGTGTCTGGGACTTGGAGGCTGGAATTTCTTCATA | 1895 |
| Db | | 1788 | TTTTGTGCGGTTCAATGAACACTGCTGGTGTCTGGGACTTGGAGGCTGGAATTTCTTCATA | 1847 |
| QY | | 1896 | TGCTGAGTTGATATTAGTGAATGTGCTGGGTTGATCTTCACAAAGGAATGATCTG | 1955 |
| Db | | 1848 | TGCTGAGTTGATATTAGTGAATGTGCTGGGTTGATCTTCACAAAGGAATGATCTG | 1907 |
| QY | | 1956 | GATGGGCTCCTTCTATGCTCCAGGCTGTGTGGGCAATTAATGTGCTGCGCTGTGACCTC | 2015 |
| Db | | 1908 | GATGGGCTCCTTCTATGCTCCAGGCTGTGTGGGCAATTAATGTGCTGCGCTGTGACCTC | 1967 |
| QY | | 2016 | CATGTACTTCCAGTGTCTGGGCGGTATGAGACACAAAGTACCCTATGAACCGCTTCAA | 2075 |
| Db | | 1968 | CATGTACTTCCAGTGTCTGGGCGGTATGAGACACAAAGTACCCTATGAACCGCTTCAA | 2027 |
| QY | | 2076 | ACGCTCCCGATCCAAACAACTCTACATGGGCTGCTGGCTGGTGTCTTCTCCAGGCT | 2135 |
| Db | | 2028 | ACGCTCCCGATCCAAACAACTCTACATGGGCTGCTGGCTGGTGTCTTCTCCAGGCT | 2087 |
| QY | | 2136 | CGTGGCGGTGGCTTACACATCAATGTCCCTCCCAACCTCCTTTGACTGGGGGCGGTTCA | 2195 |
| Db | | 2088 | CGTGGCGGTGGCTTACACATCAATGTCCCTCCCAACCTCCTTTGACTGGGGGCGGTTCA | 2147 |
| QY | | 2196 | TGGGAAAAACAAATGTAAGATGTCTCTCAAGACATTTGAAGAAAGATTTCCAACTT | 2255 |
| Db | | 2148 | TGGGAAAAACAAATGTAAGATGTCTCTCAAGACATTTGAAGAAAGATTTCCAACTT | 2207 |

QY 2256 CCTGGGCAAGATCTTTGCTTCCCTCCGCAATCCAGGCTGATCACTCCAGGCACTCTGCT 2315
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Db 2208 CCTGGGCAAGATCTTTGCTTCCCTCCGCAATCCAGGCTGATCACTCCAGGCACTCTGCT 2267
QY 2316 GATGTTCTGGCCATTTACTACCTGAATCAGATTGCCAAAAGCCTTTCCGAGCTAATGC 2375
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Db 2268 GATGTTCTGGCCATTTACTACCTGAATCAGATTGCCAAAAGCCTTTCCGAGCTAATGC 2327
QY 2376 CCAGCTGAGGAGAAAATCCAAAGTCCGTGAAGTTGAGAAAGTCACTCAAAATCTGTAA 2435
|||||
Db 2328 CCAGCTGAGGAGAAAATCCAAAGTCCGTGAAGTTGAGAAAGTCACTCAAAATCTGTAA 2387
QY 2436 AGGCAAAAGCCACAGCCAGAGATTCAAGAGACACCTAAAAGCAAGCTCCAAAAATGCCAC 2495
|||||
Db 2388 AGGCAAAAGCCACAGCCAGAGATTCAAGAGACACCTAAAAGCAAGCTCCAAAAATGCCAC 2447
QY 2496 CCAGCTCCAACTCAACAAAGAAAGACACCTCCCTCTGCCAGCCAAAGCAGGCAAT 2555
|||||
Db 2448 CCAGCTCCAACTCAACAAAGAAAGACACCTCCCTCTGCCAGCCAAAGCAGGCAAT 2507
QY 2556 GACAAAGAAAGGCGCAGGGCCCTGGGACCTCCAAATCTGCCAGCAGACCACTGCTGC 2615
|||||
Db 2508 GACAAAGAAAGGCGCAGGGCCCTGGGACCTCCAAATCTGCCAGCAGACCACTGCTGC 2567
QY 2616 CTCTGGACACCTTCTATATCTCGGCCCTTGGAAATCGAACAGATTCTGGCAGCGCCC 2675
|||||
Db 2568 CTCTGGACACCTTCTATATCTCGGCCCTTGGAAATCGAACAGATTCTGGCAGCGCCC 2627
QY 2676 ATCTCAGACTCATCCGTGAGAGTCAAGCTTGGAAAGATGCTCAGAGACCTCCCACTG 2735
|||||
Db 2628 ATCTCAGACTCATCCGTGAGAGTCAAGCTTGGAAAGATGCTCAGAGACCTCCCACTG 2687
QY 2736 ACGGCTAGGACTCAGGGAGGCTCGACCTAGGGCTGATCTCAAGTACCCAGTTTCA 2795
|||||
Db 2688 ACGGCTAGGACTCAGGGAGGCTCGACCTAGGGCTGATCTCAAGTACCCAGTTTCA 2747
QY 2796 AATACCAAAACAAGTTCTGCTCCCTCTTCTCTCAATACATGCTCTGCTCTC 2855
|||||
Db 2748 AATACCAAAACAAGTTCTGCTCCCTCTTCTCTCAATACATGCTCTGCTCTC 2807
QY 2856 TTGGATGCAATGAATTTGATTCCTCAGGCCCTTGTCAAGTACCGAAGGAAGAAAG 2915
|||||
Db 2808 TTGGATGCAATGAATTTGATTCCTCAGGCCCTTGTCAAGTACCGAAGGAAGAAAG 2867
QY 2916 TGGCTTCACTGCTCTTAAAGGAAGTGAAGCATCTCGACCTAACTGCCCTCCAAAT 2975
|||||
Db 2868 TGGCTTCACTGCTCTTAAAGGAAGTGAAGCATCTCGACCTAACTGCCCTCCAAAT 2927
QY 2976 ATCTTGGTTCAAGCAGCTTGAAACCCACGCTCAAGTGGTGAACCTTGCTCCGATTT 3035
|||||
Db 2928 ATCTTGGTTCAAGCAGCTTGAAACCCACGCTCAAGTGGTGAACCTTGCTCCGATTT 2987
QY 3036 TCGAGATTGGGAGAGGAGCCATGACACCTCGTGAATTTTCCATGGGATACAGTTTAA 3095
|||||
Db 2988 TCGAGATTGGGAGAGGAGCCATGACACCTCGTGAATTTTCCATGGGATACAGTTTAA 3047

QY 3096 GACAGGGTTTCTGCCAGCTTCCCTAACCAAGAGGGGATGAGAAAGGCTACATTCT 3155
|||||
Db 3048 GACAGGGTTTCTGCCAGCTTCCCTAACCAAGAGGGGATGAGAAAGGCTACATTCT 3107
QY 3156 CATTCAGAGGAAG 3169
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Db 3108 CATTCAGAGGAAG 3121

RESULT 3
US-10-450-763-28100
; Sequence 28100, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 28100
; LENGTH: 5027
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1906)..(2340)
; OTHER INFORMATION: 100% homologous to Homo sapiens du68c3.3 (novel
; OTHER INFORMATION: gene),accession number AL049712,Smith-Waterman Score=778.
US-10-450-763-28100

Query Match 72.4% Score 2294.6; DB 9; Length 5027;
Best Local Similarity 90.9%; Pred. No. 0;
Matches 2545; Conservative 0; Mismatches 59; Indels 195; Gaps 2;
QY 93 CACAGGTGACAGCTGGGAAAGATCCTCAACAAAGCGGCTCTCAAAAGCCAGGGAGC 152
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Db 45 CTCAGGTGACAGGCTGGGAAAGATCCTCAACAAAGCGGCTCTCAAAAGCCAGGGAGC 104
QY 153 CCCAGGACGGCCGGAGCTCAGCGAAGCAAGAGAGCGCGGGGCGAGCCCAAGCCC 212
|||||
Db 105 CCCAGGACGGCCGGAGCTCAGCGAAGCAAGAGAGCGCGGGGCGAGCCCAAGCCC 164
QY 213 GGGGCTCCCGGAGGAAGCAAAAGGGCCAGAGACACAGAAAGAGCTGGGGAGCA 272
|||||
Db 165 GGGGCTCCCGGAGGAAGCAAAAGGGCCAGAGACACAGAAAGAGCTGGGGAGCA 224
QY 273 GGAAGCGGGGAGAGCGAGAGGACCTGCGAGGGGCAAGAAAGCGGACGAGAGGGCTC 332
|||||
Db 225 GGAAGCGGGGAGAGCGAGAGGACCTGCGAGGGGCAAGAAAGCGGACGAGAGGGCTC 284

QY 333 CTTCCAGAGGAGACAGACGCCCAAAGAGGAAAAAGAGATTCGAGAGAGAGAA 392
|||||
Db 285 CTTCCAGAGGAGACAGACGCCCAAAGAGGAAAAAGAGATTCGAGAGAGAGAA 344
393 GTTCGAGGCGGAGAGAAAACCAAGTCATCCTCTTGCCCTCAAGTCCTGGTGGGA 452
|||||
Db 345 GTTCGAGGCGGAGAGAAAACCAAGTCATCCTCTTGCCCTCAAGTCCTGGTGGGA 404
453 GTCCCTGTCCGAGAGAACTGCGCCAGATCCTGAGAGAGGTGGAGAAAAAGAGCT 512
|||||
Db 405 GTCCCTGTCCGAGAGAACTGCGCCAGATCCTGAGAGAGGTGGAGAAAAAGAGCT 464
513 CATTGCACCATGCGAGAGCAAGCCTGGCCCATGGCCAAAGAAAGCTGACAGCTCAGGA 572
|||||
Db 465 CATTGCACCATGCGAGAGCAAGCCTGGCCCATGGCCAAAGAAAGCTGACAGCTCAGGA 524
573 GGCCAGGAATTTGTGAGAAATGAGAGTGCTTGAGAAAGGGGAAAGCCAGAACT 632
|||||
Db 525 GGCCAGGAATTTGTGAGAAATGAGAGTGCTTGAGAAAGGGGAAAGCCAACT 584
633 ATATGCTACAAAGATGCTGATGGCAAGAAATGGGTCAAAATTAAGAGAGCTTGATTA 692
|||||
Db 585 ATATGCTACAAAGATGCTGATGGCAAGAAATGGGTCAAAATTAAGAGAGCTTGATTA 644
693 TTTCAAGACTCAATGTATCCCTGGGAATGAGATCAAGACATTTGAAGTCACTTTGG 752
|||||
Db 645 TTTCAAGACTCAATGTATCCCTGGGAATGAGATCAAGACATTTGAAGTCACTTTGG 704
753 TTCTCACTGGCATGTATTTCACTTTTCTCCATGGATGTATGGAGTTAACCTTGTCT 812
|||||
Db 705 TTCTCACTGGCATGTATTTCACTTTTCTCCATGGATGTATGGAGTTAACCTTGTCT 764
813 TTTGGCTTAATTTGGTCACTAATCCAGAGGACT----- 854
|||||
Db 765 TTTGGCTTAATTTGGTCACTAATCCAGAGGAGATGTACATGATCCCTGAGGA 824
855 -----GATGGGCAATGCCCTATGGAGATATTCAGAAAAA 889
825 ACCCTCAGTTATGTGCAAGAGCTGGCTGGCAAGGCCCACTGGATGACAAAGTTATGTA 884
890 CAGTGCTCGGGCTGAGAGAGAAAGGCCATGGAATTTTCT----- 930
|||||
Db 885 CTTCTTTCCAACTGGATCTACGGTCTAGGTTTGACCAAGGCTACAAATTAATTGTA 944
931 ----- 930
945 GGCTGAACTGAAGAGATCCGCTTCCAGACTCACTCAATGGCTACTGGAGATCTCAGA 1004
931 ----- 930
1005 AGATCAATTTTCAGAGCTTACTCAGTGGCTCTGGCAGGCTCAGAAAACTGCTTCAA 1064
931 -----GTCTTTGGATTTTGAAGGCTATACAAAGTACTGCACTCTCTTA 977
1065 CCTTACTTATGGGCTGTTCOAAGGTTCAAGGCTATACAAAGTACTGCACTCTCTTA 1124

QY 978 TGCTACTACAAACAAGAGACATCGGCTGGTGAAGTACCGGCTGCTATGGCTTA 1037
|||||
Db 1125 TGCTACTACAAACAAGAGACATCGGCTGGTGAAGTACCGGCTGCTATGGCTTA 1184
1038 CTTTATGTGGGGGTCAAGCCTGTGGGCTACAACCTGATTAATGTCAATGCAATGGC 1097
|||||
Db 1185 CTTTATGTGGGGGTCAAGCCTGTGGGCTACAACCTGATTAATGTCAATGCAATGGC 1244
1098 CAGCAATACCAAGAGAGCAAGCGGAAGGGAGAGTGAACACTCACTCAGCTTCAA 1157
|||||
Db 1245 CAGCAATACCAAGAGAGCAAGCGGAAGGGAGAGTGAACACTCACTCAGCTTCAA 1304
1158 GATGTTACCAAGCTGGAGCTACCTGATCGGAATTCAGAGAGCTGATTAACAAATATGC 1217
|||||
Db 1305 GATGTTACCAAGCTGGAGCTACCTGATCGGAATTCAGAGAGCTGATTAACAAATATGC 1364
1218 ATCCATCAACCAAGCTTCAAGGAATCAATAGTGAATGACAGAGAGTAAACAAAGAGA 1277
|||||
Db 1365 ATCCATCAACCAAGCTTCAAGGAATCAATAGTGAATGACAGAGAGTAAACAAAGAGA 1424
1278 AATATCATCTGACAGATTTCTTGTGTCTGTGCTGGCCAACTTCTCATCATCTGCTGTT 1337
|||||
Db 1425 AATATCATCTGACAGATTTCTTGTGTGTCTGTGCTGGCCAACTTCTCATCATCTGCTGTT 1484
1338 GTTGAAGTGGGTACCTCATTTACTTTGTGTTAAGCAATCTCAGCAATTTCCAAAT 1397
|||||
Db 1485 GTTGAAGTGGGTACCTCATTTACTTTGTGTTAAGCAATCTCAGCAATTTCCAAAT 1544
1398 GAGAAATGTCAGCTGGTATGAAAGGATGAGGTAGAGTCTGATGCTGGTGAAT 1457
|||||
Db 1545 GAGAAATGTCAGCTGGTATGAAAGGATGAGGTAGAGTCTGATGCTGGTGAAT 1604
1458 GTTTGTCCCTCTGTTTGAAACCATGCTGCCCTGGAGAAATTACACCAACCACTGG 1517
|||||
Db 1605 GTTTGTCCCTCTGTTTGAAACCATGCTGCCCTGGAGAAATTACACCAACCACTGG 1664
1518 ACTGAAGTGGCAGCTGGAGAGCACTTTGCACTTCTCTGGGAAACCTCTACACATTTCT 1577
|||||
Db 1665 ACTGAAGTGGCAGCTGGAGAGCACTTTGCACTTCTCTGGGAAACCTCTACACATTTCT 1724
1578 CTTGGCCCTGATGATGACGTCACCTCAAGCTTGCTAATGAGAGACATTAAGAAACAT 1637
1725 CTTGGCCCTGATGATGACGTCACCTCAAGCTTGCTAATGAGAGACATTAAGAAACAT 1784
1638 CACTCACTGACCTGTGTTAACTATTACAACTTTCTGGTGAAGAGAGTGTCCCCG 1697
|||||
Db 1785 CACTCACTGACCTGTGTTAACTATTACAACTTTCTGGTGAAGAGAGTGTCCCCG 1844
1698 ACCAACCCCTGACACCTGCAATGTGCCCGGGGTTCTGCTGGGAGACAGCTGTGGCAT 1757
|||||
Db 1845 ACCAACCCCTGACACCTGCAATGTGCCCGGGGTTCTGCTGGGAGACAGCTGTGGCAT 1904
1758 TGAATTCATGAGGCTGACGGTGTCTGACATGCTGGTAAAGTACATCAATCCTGCTGG 1817
|||||
Db 1905 TGAATTCATGAGGCTGACGGTGTCTGACATGCTGGTAAAGTACATCAATCCTGCTGG 1964
1818 GGACTTCTTACAGGAGCTGTTTGTGGGTTTCAATGAATACTGCTGGTGGAGCTTGA 1877

Db 1965 GGAATTCTACGGGGCTGTGTTGTGGGTTCACTGAAGTCTAGTGGTGGGACTGGA 2024
QY 1878 GGCTGGATTTCCTCATATGCTGAGTTGATATTAAGTGGAAATGGCTGGGTTGATCTT 1937
Db 2025 GGCTGGATTTCCTCATATGCTGAGTTGATATTAAGTGGAAATGGCTGGGTTGATCTT 2084
QY 1938 CAACCAAGGAATGATGTGATGGGCTCCTTCTATGCTCCAGGGCTGGTGGGCAATTAATGT 1997
Db 2085 CAACCAAGGAATGATGTGATGGGCTCCTTCTATGCTCCAGGGCTGGTGGGCAATTAATGT 2144
QY 1998 GCTGGCCTGCTGACCTCATGATCTTCAAGTGGTGGGGGTGATGAGACAGCAATACC 2057
Db 2145 GCTGGCCTGCTGACCTCATGATCTTCAAGTGGTGGGGGTGATGAGACAGCAATACC 2204
QY 2058 CCATGACGGGTGTTCAAAAGCTCCCGATCCAAACAATTCTAATGGGGCTGCTGCTGCT 2117
Db 2205 CCATGACGGGTGTTCAAAAGCTCCCGATCCAAACAATTCTAATGGGGCTGCTGCTGCT 2264
QY 2118 GGTGCTCTTCTCAGGCTCCTGCGGGTGGCTACACCATCATGTCCCTCCACCTCCTT 2177
Db 2265 GGTGCTCTTCTCAGGCTCCTGCGGGTGGCTACACCATCATGTCCCTCCACCTCCTT 2324
QY 2178 TGAAGTGGGGCCCTTCAGTGGGAAAAACAGAAATGTACGATGCTCCAGAGACATTTGA 2237
Db 2325 TGAAGTGGGGCCCTTCAGTGGGAAAAACAGAAATGTACGATGCTCCAGAGACATTTGA 2384
QY 2238 AAACGATTTCCCAACCTTCTGGGGCAAGATCTTTGCTTCTCCCAATCCAGGCTGAT 2297
Db 2385 AAACGATTTCCCAACCTTCTGGGGCAAGATCTTTGCTTCTCCCAATCCAGGCTGAT 2444
QY 2298 CATCCAGCCATCTGCTGATGTTCTTGGCCATTTACTAAGTGAATCAAGTTCCAAAG 2357
Db 2445 CATCCAGCCATCTGCTGATGTTCTTGGCCATTTACTAAGTGAATCAAGTTCCAAAG 2504
QY 2358 CTTTCCCGAGCTAATGCCAGCTGAGAGAAAGAAATCCAAAGTGGTGGAGTTGAGAA 2417
Db 2505 CTTTCCCGAGCTAATGCCAGCTGAGAGAAAGAAATCCAAAGTGGTGGAGTTGAGAA 2564
QY 2418 GAGTCACAAATCTGTAAAGGCAAAAGCCAGCCAGATTCAGAGGACACACTAAAG 2477
Db 2565 GAGTCACAAATCTGTAAAGGCAAAAGCCAGCCAGATTCAGAGGACACACTAAAG 2624
QY 2478 CAGCTCCAAAAATGCCACCAAGCTCCAACTCAAGAGAGAGACACTCCTCCTCTGC 2537
Db 2625 CAGCTCCAAAAATGCCACCAAGCTCCAACTCAAGAGAGAGACACTCCTCCTCTGC 2684
QY 2538 CAGCCAAAGCAAGCCATGAGCAAGAAAGGCGAGGGCTGGAGACTCCAAATTCGCCAG 2597
Db 2685 CAGCCAAAGCAAGCCATGAGCAAGAAAGGCGAGGGCTGGAGACTCCAAATTCGCCAG 2744
QY 2598 CAGGACCACTGCTGCTGCTGAGCACTTCTATATCTCGGGCCCTTGGAAATCGAGCC 2657
Db 2745 CAGGACCACTGCTGCTGCTGAGCACTTCTATATCTCGGGCCCTTGGAAATCGAGCC 2804
QY 2658 AGATTCTGGCCACGCCCATCTCAGACTCAATCCGTGAG 2696

Db 2805 AGATTCTGGCCACGCCCATCTCAGACTCAATCCGTGAG 2843
RESULT 4
US-10-115-831-134
; Sequence 134, Application US/10115831 Publication date 11/27/03
; Publication No. US20030219743A1
; GENERAL INFORMATION:
; APPLICANT: Teng, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyun
; APPLICANT: Drmanec, Radoje T.
; TITLE OF INVENTION: No. US20030219743A1el Nucleic Acids and
; FILE REFERENCE: 792CIP2ADIV
; CURRENT APPLICATION NUMBER: US/10/115,831
; PRIOR APPLICATION NUMBER: 2002-04-02
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ. ID NOS: 178
; SOFTWARE: pt_Fl_genes Version 2.0
; SEQ. ID NO 134
; LENGTH: 4895
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4785)
US-10-115-831-134
Query Match 72.4%; Score 2293; DB 6; Length 4895;
Best Local Similarity 90.9%; Pred. No. 0;
Matches 2544; Conservative 0; Mismatches 60; Indels 195; Gaps 2;
QY 93 CACAGGTGACAGGCTGGGAAAGAGATCCTCAAGCAAGCGGGCTCTCAAAAGCCAGGGGAC 152
Db 45 CTGAGGTGACAGGCTGGGAAAGAGATCCTCAAGCAAGCGGGCTCTCAAAAGCCAGGGGAC 104
QY 153 CCGAGGAGGGCGGAGGCTCAGCGGAAGGCAAGAGAGGGCGCGGGGACGCCACGCC 212
Db 105 CCGAGGAGGGCGGAGGCTCAGCGGAAGGCAAGAGAGGGCGCGGGGACGCCACGCC 164
QY 213 GGGGCTCTCCCGAGAGAAAGCAAGGAGGCGAGAGACAGAGAAAGACTGGGGAGCA 272
Db 165 GGGGCTCTCCCGAGAGAAAGCAAGGAGGCGAGAGACAGAGAAAGACTGGGGAGCA 224
QY 273 GGAAGGGGGGAGAGAGAGAGACTGCGAGAGGCGAGAGAAAGCGGACAGAGGGCTC 332
Db 225 GGAAGGGGGGAGAGAGAGAGACTGCGAGAGGCGAGAGAAAGCGGACAGAGGGCTC 284
QY 333 CTTCCAGAGCGGACAGAGCGCCCAAGAGGAGAAAGAGATTCCAGGAAAGAGAGAA 392
Db 285 CTTCCAGAGCGGACAGAGCGCCCAAGAGGAGAAAGAGATTCCAGGAGAGAGAA 344

| | | | |
|----|------|--|-------|
| Db | 1185 | CTTTATGGTGGGGGTGAGCGGTGTGGCTTACAGCCTGATTTATGTCACTTCATGCAATGCG | 12444 |
| OY | 1098 | CAGCATATACCAAGGAGCAGCGGAGGGGAGGTGAACAATTCAATTCACTGACTTCA | 11577 |
| Db | 1245 | CAGCATATACCAAGGAGCAGCGGAGGGGAGGTGAACAATTCAATTCACTGACTTCA | 13044 |
| OY | 1158 | GATGTTCACACGCTGGGAGCTACGTGATCGGGGAATTCAGAGACGTGATTAACAAATATCG | 12171 |
| Db | 1305 | GATGTTCACACGCTGGGAGCTACGTGATCGGGGAATTCAGAGACGTGATTAACAAATATCG | 13664 |
| OY | 1218 | ATCATCAGCACACACTTCAAGGAATCATAGTGGATGAACAAGAGGTAAACAAAGAGA | 12777 |
| Db | 1365 | ATCATCAGCACACACTTCAAGGAATCATAGTGGATGAACAAGAGGTAAACAAAGAGA | 14244 |
| OY | 1278 | AAATATCATCTGACAGAGATTTCTTCGTGTCTGGCCACTTGTCAATCATGCTGTTT | 13373 |
| Db | 1425 | AAATATCATCTGACAGAGATTTCTTCGTGTCTGGCCACTTGTCAATCATGCTGTTT | 14844 |
| OY | 1338 | GTGTGGAGGGGTACCTCAATTACTTTGGGTTAAGCAATCTCAGCAATTCGCMAAAT | 13977 |
| Db | 1485 | GTGTGGAGGGGTACCTCAATTACTTTGGGTTAAGCAATCTCAGCAATTCGCMAAAT | 15444 |
| OY | 1398 | CGAAGATGTCACTGTGATGAAGAGATGAGGTAGAGATCGTGAATCCCTGCTTGGAAT | 14577 |
| Db | 1545 | CGAAGATGTCACTGTGATGAAGAGATGAGGTAGAGATCGTGAATCCCTGCTTGGAAT | 16044 |
| OY | 1458 | GTTTTGTCCCCCTGTGTTGAACCATCGTGCCTCGGAGAAATTACACCCACGACGTGG | 15171 |
| Db | 1605 | GTTTTGTCCCCCTGTGTTGAACCATCGTGCCTCGGAGAAATTACACCCACGACGTGG | 16644 |
| OY | 1518 | ACTGAAGTGGCAGCTGGGAGGAGCATCTTTGCACTCTTCTGTGGGAACCTCTACACATTTCT | 15777 |
| Db | 1665 | ACTGAAGTGGCAGCTGGGAGGAGCATCTTTGCACTCTTCTGTGGGAACCTCTACACATTTCT | 17244 |
| OY | 1578 | CTTGGCCCTGATGATGATGACGTCCACACTCAACGTTGCTAATGAAGAGCAATTAAGAACT | 16377 |
| Db | 1725 | CTTGGCCCTGATGATGATGACGTCCACACTCAACGTTGCTAATGAAGAGCAATTAAGAACT | 17844 |
| OY | 1638 | CACGTCACTGGACTGTGTTTAACATTAACAACCTTCTGTGTGAACGAGGTGTCCCCG | 16977 |
| Db | 1785 | CACGTCACTGGACTGTGTTTAACATTAACAACCTTCTGTGTGAACGAGGTGTCCCCG | 18444 |
| OY | 1698 | ACCAACCCCTGCAACCTCGAAGATGTGTCCCGGGGTTCTTCTGTGGAGACGCTGTGGGCAAT | 17577 |
| Db | 1845 | ACCAACCCCTGCAACCTCGAAGATGTGTCCCGGGGTTCTTCTGTGGAGACGCTGTGGGCAAT | 19044 |
| OY | 1758 | TGAATATATAGAGGCTGACCGGTGTCTGACATGCTGGTAAGTACATCAACAATCTCTGTGGG | 18171 |
| Db | 1905 | TGAATATATAGAGGCTGACCGGTGTCTGACATGCTGGTAAGTACATCAACAATCTCTGTGGG | 19644 |
| OY | 1818 | GGAATCTTACAGGGGTGTGTTGTGTGGGTTCAACAATCACTGCTGGTGGAGCACTTGA | 18777 |
| Db | 1965 | GGAATCTTACAGGGGTGTGTTGTGTGGGTTCAACAATCACTGCTGGTGGAGCACTTGA | 20244 |
| OY | 1878 | GGCTGGAATTCCTTCATATGCTGAAGTTGAATTAAGGAAATGTGCTGGGTTGAATCTT | 19377 |

Db 2025 GGCTGGATTTCCTTCATATAGCTGAGTTTGANATTAAGTGAATAATGTGGAAATGTGCTGGGTTTGAATCTT 2084
QY 1938 CAACCAAGAAATGATGTGATGATGGCTCTTCTATGCTCCAGGCTGGTGGGCAATTAATGT 1997
Db 2085 CAACCAAGAAATGATGTGATGATGGCTCTTCTATGCTCCAGGCTGGTGGGCAATTAATGT 2144
QY 1998 GCTGGGCTCTGCTGACTCCATGATGATCTTCAAGTGGTGGGCGGTGATGAGACGACGTAAC 2057
Db 2145 GCTGGGCTCTGCTGACTCCATGATGATCTTCAAGTGGTGGGCGGTGATGAGACGACGTAAC 2204
QY 2058 CCATGAAGCGCTGTGAAGAGCTCCGATCCGAACTCTTCAATGAGGCTCTCTGCTGCT 2117
Db 2205 CCATGAAGCGCTGTGAAGAGCTCCGATCCGAACTCTTCAATGAGGCTCTCTGCTGCT 2264
QY 2118 GGTGCTCTTCTCTAGGCTCTGAGCGGTGGCTACACCATCATGTCCTCCCAAGCTCTT 2177
Db 2265 GGTGCTCTTCTCTAGGCTCTGAGCGGTGGCTACACCATCATGTCCTCCCAAGCTCTT 2224
QY 2178 TGACTGGGGCGCTTCAGTGGGAAACAGAAATGTACGATGCTCTCCAGAGACATTTGA 2237
Db 2325 TGACTGGGGCGCTTCAGTGGGAAACAGAAATGTACGATGCTCTCCAGAGACATTTGA 2384
QY 2238 AAACGATTTCCAAACCTTCCTGGGGAAGATCTTGGCTTCCTGGGCAATCCAGGCTGAT 2297
Db 2385 AAACGATTTCCAAACCTTCCTGGGGAAGATCTTGGCTTCCTGGGCAATCCAGGCTGAT 2444
QY 2298 CATCCAGCATCTGCTGATGTTCTTGGCAATTTACTACCTGAACCTCAGTTTCCAAAG 2357
Db 2445 CATCCAGCATCTGCTGATGTTCTTGGCAATTTACTACCTGAACCTCAGTTTCCAAAG 2504
QY 2358 CTTTCCGAGCTAATGCCAGCTGAGGAGGAAATCCAAAGCTCCGTGAAATTGAGAA 2417
Db 2505 CTTTCCGAGCTAATGCCAGCTGAGGAGGAAATCCAAAGCTCCGTGAAATTGAGAA 2564
QY 2418 GAGTCACAAATCTGTAAAGGCAAGGCCAGGCCAGATGAGAGGACACACTAAAG 2477
Db 2565 GAGTCACAAATCTGTAAAGGCAAGGCCAGGCCAGATGAGAGGACACACTAAAG 2624
QY 2478 CAGCTCCAAAAATGCCACCCAGCTCCAACTCACAGAGGAAAGACACACTCCCTCTGC 2537
Db 2625 CAGCTCCAAAAATGCCACCCAGCTCCAACTCACAGAGGAAAGACACACTCCCTCTGC 2684
QY 2538 CAGCCAAAGCCAGGCCATGACAAAGAAAGGCGAGGCGCTGGAGCTCCAAATTCGCAAG 2597
Db 2685 CAGCCAAAGCCAGGCCATGACAAAGAAAGGCGAGGCGCTGGAGCTCCAAATTCGCAAG 2744
QY 2598 CAGGACCACACTGCTGCTCTGGACACTTCTATATCTCGGCCCCCTGAAATCGAGC 2657
Db 2745 CAGGACCACACTGCTGCTCTGGACACTTCTATATCTCGGCCCCCTGAAATCGAGC 2804
QY 2658 AGATTCTGGCCACGCCCATCTCAGACTCATCCCTGGAG 2696
Db 2805 AGATTCTGGCCACGCCCATCTCAGACTCATCCCTGGAG 2843

RESULT 5
US-10-487-887-7

; Sequence 7, Application US/10487887
; Publication No. US20040249139A1
; GENERAL INFORMATION:
; APPLICANT: Griffith, Andrew J
; APPLICANT: Kurime, Kiyoto
; APPLICANT: Wileox, Edward
; APPLICANT: Friedman, Thomas
; TITLE OF INVENTION: TRANSDUCTIN-1 AND TRANSDUCTIN-2 AND APPLICATIONS TO
HEREDITARY
; TITLE OF INVENTION: DEAFNESS
; FILE REFERENCE: 226544
; CURRENT APPLICATION NUMBER: US/10/487,887
; PRIOR FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/US02/29614
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/323,275
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 3216
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-487-887-7

Query Match 61.8%; Score 1957.6; DB 8; Length 3216;
Best Local Similarity 83.7%; Pred. No. 0;
Matches 2241; Conservative 0; Mismatches 429; Indels 6; Gaps 2;

QY 96 AGGTGACAGCTTGGGAGAGAGATCTCAAGCAAGCGGCTCTCAAGCCGAGGGAGCCCC 155
Db 354 AGGTGACAGCTTGGGAGAGAGATCTCAAGCAAGCGGCTCTCAAGCCGAGGGAGCCCC 413
QY 156 AGGAGGGGAGGAGCTCAGCGAAGCGAAGAGGAGCGCGGGGCGAGCCCAAGCCGG 215
Db 414 AGGAGGGGAGGAGCTCAGCGAAGCGAAGAGGAGCGCGGGGCGAGCCCAAGCCGG 473
QY 216 GTCTCCCGAGAGAAACAGAGGCGCAGAGACACAGAGAGAGCTGGGGAGCAGGA 275
Db 474 GTCTCCCGAGAGAAACAGATGGAAATGGAACTATCACAAAGGGTTCCAGGGACAGAA 533
QY 276 GGGGGGAGGAGGAGGAGGAGCTGGAGGCCAGAGAAAGCGGAGAGAGGGGCTCTT 335
Db 534 ACCAGAAAGGTGAGAGGCTCTACAGGGGAGAAAG---GACCGAGAACTTCCCT 590
QY 336 CCAAGAGCGGACAGAGCCCAAGAGGAAAGAGATTCCAGAGAGAGAGAAATC 395
Db 591 TAAAGAGCAGAGAGATCTCAAGAGAGAGAGGAGGCTCTAGAGAGAGG---CAGG 647
QY 396 GAAAGGACAGAAACCAAGGTCACTCTCTTGGCTTCCAGTGGCTCTGGTGGGAGTC 455
Db 648 CAGGACCTGAGAAACCAAGGTCCACTTCTGGGCTCCAGTGTCTCTACTGGAGACTC 707
QY 456 CCGTCCGAGAGAGAGAGCTGGCCCAAGATCTGAGGACGAGTGAAGAAAGAAAGCTCAT 515
Db 708 CCGTCCGAGAGAGAGAGCTGGCCCAAGATCTGAGGACGAGTGAAGAAAGAAAGCTCAT 767

| | | | |
|----|------|---|------|
| Ds | 1608 | CATTACTTTGTGGAAACGGTCCAGAGATTCTCCAAAATGCAAAATGTCACTGGTA | 1667 |
| QY | 1416 | TGAAGAAAGAGGTAGAAGATGGTAGTCCCTGGTTGGAAATGTTTTGTCCCCCTCGTT | 1475 |
| Ds | 1668 | TGAAGAAATGAGGTGAGATGGTAGTGTCTTGGTAGGGATGTTTTGTCCCCCTCGTT | 1727 |
| QY | 1476 | TGAAGCAATGGCTGCCCTGGAAATATACACCACGCACTGGACTGAATGGCACTGGG | 1535 |
| Ds | 1728 | TGAAGCAATGGCTGCCCTGGAAATATACACCACGCACTGGGCTGAATGGCACTGGG | 1787 |
| QY | 1536 | AGCAATCTTGGACCTTCCGTGGGGAACCTACACATTTCTTGGCCCGTATGGATGA | 1595 |
| Ds | 1788 | CCGACATCTTGGCCCTTCTCCTGGAAACCTACACGTTTCTCCTGGCCCTATGGACAA | 1847 |
| QY | 1596 | CGTCACTCAAGCTTGGTAAATGAAGACATAAAGACATCACTCACTGGACTGTT | 1655 |
| Ds | 1848 | TGTCACTCAATTAAGCTTCTTAATGAGGAAAAATCAAGACATCACTCACTGGACCTGTT | 1907 |
| QY | 1656 | TACATATTACAACCTCTCTGGTGGAAACAGAGTGTCCCGACACACCCCTGGACCCCTG | 1715 |
| Ds | 1908 | TACATATTACAATCTCTCAGGTGGAAATGAGAGTGTCCCGACACACACACCTG | 1967 |
| QY | 1716 | AAGTGTGCCCGGGGTTCTTGGTGGGAGACAGCTGTGGGCAATGAATTCATGAGGCTAC | 1775 |
| Ds | 1968 | AAGTGTGCCCGAGGTTCTTGGTGGGAGACAGCTGTGGGCAATGAATTCATGAGGCTAC | 2027 |
| QY | 1776 | GGTGTCTGACATGCTGGTAACTACATCAACATCTCTCTGGGGGACTCTCAACGGGCTTG | 1835 |
| Ds | 2028 | CGTGTCTGACATGCTGGTAACTACATCAACATCTCTCTGGGGGAAATTCCTCCAGGCTTG | 2087 |
| QY | 1836 | TTTTGTCCGGTTCATGAACACTGCTGGTGGCTGGGACCTTGAAGGCTGAATTCCTCATTA | 1895 |
| Ds | 2088 | TTTTGTCCGGTTCATGAACACTGCTGGTGGCTGGGACCTTGAAGGCTGAATTCCTCATTA | 2147 |
| QY | 1896 | TGCTGAATGTAATATAGTGAATAATGTCTGGGTTTGATCTTCAACCAAGAAATGATCTG | 1955 |
| Ds | 2148 | TGCTGAATGTAATATAGTGAATAATGTCTGGGTTTGATCTTCAACCAAGAAATGATCTG | 2207 |
| QY | 1956 | GATGGGGCTCCTTCTATCTCTCAAGGCTGGTGGGCAATATGTCTGGGCGGCTGACCTC | 2015 |
| Ds | 2208 | GATGGGGCTCCTTCTATCTCTCAAGGCTGGTGGGCAATATGTCTGGGCGGCTGACCTC | 2267 |
| QY | 2016 | CATGTACTTCCAGTGTCTGGGCGGTTGATGAGACGACAGTACCOCATGAACGGGTGTTCAA | 2075 |
| Ds | 2268 | CATGTACTTCCAGTGTCTGGGCGGTTGATGAGACGACAGTACCOCATGAACGGGTGTTCAA | 2327 |
| QY | 2076 | AACCTCCCAATCAACAACTTCTACATGGGCTCCTGTGCTGGTGTCTTCTCAAGCTT | 2135 |
| Ds | 2328 | AACCTCCCAATCAACAACTTCTACATGGGCTCCTGTGCTGGTGTCTTCTCAAGCTT | 2387 |
| QY | 2136 | CGTGGCGGTGGCTACACATCATGTCCCTCCACACCTCTTTTACTGGGGGCGGTTCAAG | 2195 |
| Ds | 2388 | CGTGGCGGTGGCTACACATCATGTCTCTCCACACCTCTTTTACTGGGGGCGGTTCAAG | 2447 |
| QY | 2196 | TGGGAAAAACGAATGTACATGTCTCCAGAGACCAATGAAAAGATTTTCCACACTT | 2255 |

Db 2448 TGGGAAAAAGATGTAGATGTCTCCATGAGACCATGAGAACATTTCCCTAAATT 2507
QY 2256 CTGGGCAAGATCTTTGCTTCTCGCAATCGAGGCTGATCATCCAGCCATCTGCT 2315
Db 2508 CTGGGCAAGATCTTTGCTTCTCGCAATCGAGGCTGATCATCCAGCCATCTGCT 2367
QY 2316 GATGTTCTGGCCATTACTACTGAACTCAAGATTTCCAAAAGCCTTTCCGAGCTAAATGC 2375
Db 2568 AATGTTCTGGCCATTACTACTGAACTCAAGATTTCCAAAAGCCTTTCTAGAGCTAAATGC 2627
QY 2376 CCAGCTGAGAGAAATCCAAAGTCCCTGGAATTGAGAAAGTCAAAAATCTGTA 2435
Db 2628 CCAGCTGAGAGAAATCCAAAGTCCCTGGAATTGAGAAAGTCAAAAATCTGTA 2687
QY 2436 AGGCAAAAGCCAGAGGATTCAGAGGACACACTAAAAGAGCTCCAAAATGCGAC 2495
Db 2688 GGGAAAGCCATAGTCACTATTCAAGGACACAGATCAAGAAAGCTCCAAAATGCGAC 2747
QY 2496 CCAGCTCCAACTCACCAGAGAGACACTCTCTCTGCGAGCCAAAGCCAGCCAT 2555
Db 2748 CCAGATACATCTTACTAAAAGAGCCACATCTCACTCTTCCAGCCAAATCCAGCCCT 2807
QY 2556 GAGCAAGAGGCGCAGGCGCTGAGACTCCAAATTTGCGAGCAGAGACACTGCTGCG 2615
Db 2808 GAGCAAGAGGCGCAGGCGCTGAGACTCCAAATTTGCGAGCAGAGACACTGCTGCG 2867
QY 2616 CTCTGGACACCTTCTATATCTCGGCGCCCTGGAATCGAACGATTTGCGCAGCGCCC 2675
Db 2868 CTCTGGACACCTTCTATATCTCGGCGCCCTGGAATCGAACGATTTGCGCAGCGCCA 2927
QY 2676 ATTCAGACTCATCCGTGAGAGTCAAGCTCTGGAAGAGTCTCAAGAGCTCCCACTG 2735
Db 2928 GTCTCAGACTTACACAGGCAAGTCACTCTGGAAGAGACCCAGGCTCAAGACTG 2987
QY 2736 ACAGGCTAGACTCAGAGGAGGCTGAGCCCTAGGAGCT 2771
Db 2988 ATTTCTGGCAATTCATGGGTGTCAGATCTTGGCT 3023

Search completed: November 30, 2005, 13:27:54
Job time : 2233 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 30, 2005, 06:28:46 ; Search time 254 Seconds
(without alignments)
3881.591 Million cell updates/sec

Title: US-10-792-307-3
Perfect score: 3169
Sequence: 1 gcagtcgtcgtcaccaagag.....attctcatccagaggaag 3169

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3289866 seqs, 155557593 residues
Total number of hits satisfying chosen parameters: 6579732

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA_New**
1: /cgn2_6/ptodate/1/pubpna/US09_NEW_PUB.seq**
2: /cgn2_6/ptodate/1/pubpna/US06_NEW_PUB.seq**
3: /cgn2_6/ptodate/1/pubpna/US07_NEW_PUB.seq**
4: /cgn2_6/ptodate/1/pubpna/US08_NEW_PUB.seq**
5: /cgn2_6/ptodate/1/pubpna/PCT_NEW_PUB.seq**
6: /cgn2_6/ptodate/1/pubpna/US10_NEW_PUB.seq**
7: /cgn2_6/ptodate/1/pubpna/US11_NEW_PUB.seq**
8: /cgn2_6/ptodate/1/pubpna/US11_NEW_PUB.seq3**
9: /cgn2_6/ptodate/1/pubpna/US11_NEW_PUB.seq3**
10: /cgn2_6/ptodate/1/pubpna/US60_NEW_PUB.seq**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB ID | Description |
|------------|-------|-------|--------|-------|---------------------|
| c 1 | 106.8 | 3.4 | 1559 | 6 | US-10-750-185-45753 |
| 2 | 104.6 | 3.3 | 1177 | 7 | US-11-102-240-129 |
| c 3 | 62 | 2.0 | 1611 | 6 | US-10-750-185-52663 |
| 4 | 42.8 | 1.4 | 774 | 6 | US-10-750-185-36837 |
| c 5 | 42.2 | 1.3 | 2201 | 6 | US-10-821-234-91 |
| 6 | 40 | 1.3 | 2031 | 7 | US-11-135-855-5 |
| 7 | 40 | 1.3 | 2154 | 7 | US-11-135-855-6 |
| 8 | 39.8 | 1.3 | 1280 | 6 | US-10-750-185-32786 |

OM nucleic - nucleic search, using sw model

Run on: November 30, 2005, 04:49:06 ; Search time 11159 Seconds
(without alignments)
13286.877 Million cell updates/sec

Title: US-10-792-307-3
Perfect score: 3169
Sequence: 1 gcaatgcctgcacacagag.....attccatcacagagagag 3169

Scoring table: IDENTITY NUC
Gapop 10-0 , Gapext 1.0

Searched: 41078325 seqs, 2339354128 residues
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------------|--------------------|
| 1 | 606.4 | 19.1 | 1827 | 10 AY406224 | AY406224 Homo sapi |
| 2 | 452.8 | 14.3 | 1827 | 10 AY406226 | AY406226 Mus muscu |
| 3 | 435 | 13.7 | 11482 | 4 HSM80678 | BX640632 Homo sapi |
| 4 | 362.4 | 11.4 | 740 | 5 BU262560 | BU262560 603174318 |
| 5 | 327.6 | 10.3 | 450 | 3 BM482906 | BM482906 535995 MA |
| 6 | 274 | 8.6 | 595 | 11 DQ031957 | DQ031957 Homo sapi |
| 7 | 274 | 8.6 | 1656 | 4 AK016832 | AK016832 Mus muscu |

| | | | | | |
|----|------|-----|--------|-----------------------|-------------------|
| 9 | 39.6 | 1.2 | 5468 | 6 US-10-821-234-49 | Sequence 49, Appl |
| 10 | 38.8 | 1.2 | 1600 | 6 US-10-750-185-57179 | Sequence 57179, A |
| 11 | 38.6 | 1.2 | 1211 | 6 US-10-750-185-51604 | Sequence 51604, A |
| 12 | 38.6 | 1.2 | 3301 | 6 US-10-750-185-42771 | Sequence 42771, A |
| 13 | 37.8 | 1.2 | 207908 | 7 US-11-112-908-21 | Sequence 21, Appl |
| 14 | 37.8 | 1.2 | 212805 | 7 US-11-112-908-19 | Sequence 19, Appl |
| 15 | 37.6 | 1.2 | 1670 | 6 US-10-131-826A-325 | Sequence 325, App |
| 16 | 37.6 | 1.2 | 155515 | 7 US-11-112-908-42 | Sequence 42, Appl |
| 17 | 37.6 | 1.2 | 159660 | 7 US-11-112-908-43 | Sequence 43, Appl |
| 18 | 37.2 | 1.2 | 2952 | 6 US-10-689-742-211 | Sequence 211, App |
| 19 | 36.8 | 1.2 | 3122 | 6 US-10-750-185-38196 | Sequence 38196, A |
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| 21 | 36.6 | 1.2 | 1932 | 7 US-11-137-465-21 | Sequence 21, Appl |
| 22 | 36.6 | 1.2 | 1962 | 7 US-11-137-465-22 | Sequence 22, Appl |
| 23 | 36.6 | 1.2 | 166111 | 7 US-11-112-908-47 | Sequence 47, Appl |
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| 25 | 36.2 | 1.1 | 1278 | 6 US-10-750-185-45421 | Sequence 45421, A |
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| 27 | 35.4 | 1.1 | 636 | 6 US-10-821-234-615 | Sequence 615, App |
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| 29 | 35.2 | 1.1 | 1300 | 6 US-10-750-185-35427 | Sequence 35427, A |
| 30 | 35.2 | 1.1 | 1412 | 6 US-10-821-234-266 | Sequence 266, App |
| 31 | 35.2 | 1.1 | 1893 | 6 US-10-750-185-35288 | Sequence 35288, A |
| 32 | 34.8 | 1.1 | 3671 | 6 US-10-131-826A-141 | Sequence 141, App |
| 33 | 34.8 | 1.1 | 48000 | 7 US-11-159-597-20 | Sequence 20, Appl |
| 34 | 34.6 | 1.1 | 1185 | 6 US-10-750-185-53063 | Sequence 53063, A |
| 35 | 34.6 | 1.1 | 1786 | 6 US-10-750-185-46643 | Sequence 46643, A |
| 36 | 34.6 | 1.1 | 4025 | 6 US-10-750-185-61944 | Sequence 61944, A |
| 37 | 34.4 | 1.1 | 172147 | 7 US-11-112-908-22 | Sequence 22, Appl |
| 38 | 34.4 | 1.1 | 188682 | 7 US-11-112-908-23 | Sequence 23, Appl |
| 39 | 34.2 | 1.1 | 767 | 6 US-10-750-185-26125 | Sequence 26125, A |
| 40 | 34.2 | 1.1 | 1134 | 6 US-10-750-185-26390 | Sequence 26390, A |
| 41 | 34.2 | 1.1 | 1229 | 6 US-10-821-234-171 | Sequence 171, App |
| 42 | 34 | 1.1 | 6139 | 6 US-10-401-368B-25 | Sequence 25, Appl |
| 43 | 33.8 | 1.1 | 165883 | 7 US-11-112-908-18 | Sequence 18, Appl |
| 44 | 33.8 | 1.1 | 600 | 6 US-10-750-185-1686 | Sequence 1686, Ap |
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| 20 | 208 | 6.6 | 644 | 2 | BB624822 | BB624822 |
| 21 | 206.8 | 6.5 | 633 | 10 | AY404863 | AY404863 |
| 22 | 201.4 | 6.4 | 1770 | 10 | AY406225 | AY406225 |
| 23 | 198 | 6.2 | 676 | 1 | BB024587 | BB024587 |
| 24 | 170.4 | 5.4 | 597 | 11 | DE054410 | DE054410 |
| 25 | 166.6 | 5.3 | 566 | 3 | BM106641 | BM106641 |
| 26 | 162.4 | 5.1 | 739 | 7 | CK471553 | CK471553 |
| 27 | 162 | 5.1 | 549 | 9 | CE013571 | CE013571 |
| 28 | 157.2 | 5.0 | 583 | 3 | BP370498 | BP370498 |
| 29 | 143.4 | 4.5 | 1081 | 11 | CN50568N | CN50568N |
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| 33 | 128 | 4.0 | 756 | 9 | A2844449 | A2844449 |
| 34 | 124.8 | 3.9 | 266 | 1 | A1559067 | A1559067 |
| 35 | 124.6 | 3.9 | 1092 | 8 | DN708339 | DN708339 |
| 36 | 122.8 | 3.9 | 413 | 9 | AQ042815 | AQ042815 |
| 37 | 118.4 | 3.7 | 2394 | 4 | AK033447 | AK033447 |
| 38 | 117.2 | 3.7 | 315 | 1 | A1556364 | A1556364 |
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| 40 | 116.4 | 3.7 | 645 | 2 | BB624826 | BB624826 |
| 41 | 113.2 | 3.6 | 829 | 9 | BH399926 | BH399926 |
| 42 | 113 | 3.6 | 1171 | 10 | CL645372 | CL645372 |
| 43 | 113 | 3.6 | 1245 | 10 | CL641086 | CL641086 |
| 44 | 112.4 | 3.5 | 605 | 9 | A2897611 | A2897611 |
| 45 | 110.8 | 3.5 | 312 | 11 | DE042910 | DE042910 |

ALIGNMENTS

| | | | | | | |
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| RESULT 1 | | | | | | |
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| LOCUS | Homo sapiens TMC2 gene, VIRTUAL TRANSCRIPT, partial sequence, | | | | | |
| DEFINITION | genomic survey sequence. | | | | | |
| ACCESSION | AY406224.1 | GI:39762198 | | | | |
| VERSION | AY406224.1 | GI:39762198 | | | | |
| KEYWORDS | GSS. | | | | | |
| SOURCE | Homo sapiens (human) | | | | | |
| ORGANISM | Homo sapiens | | | | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | |
| | Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini; | | | | | |
| REFERENCE | 1 (bases 1 to 1827) | | | | | |

| | |
|---|--|
| AUTHORS | Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J., Adams,M.D. and Cargill,M. |
| TITLE | Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios |
| JOURNAL | Science 302 (5652), 1960-1963 (2003) |
| PUBMED | 14671302 |
| REFERENCE | 2 (bases 1 to 1827) |
| AUTHORS | Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J., Adams,M.D. and Cargill,M. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA |
| COMMENT | This sequence was made by sequencing genomic exons and ordering them based on alignment. |
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| QY | 1049 GGGTCAGCGTGTTCGGCTACAGCTGATTATGTCATTGATCGATGCCAGCATACC 1108 |
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| DB | 140 NNN 199 |
| QY | 1109 AAGGAAGCAGACGCGAGAGAGTGCACATTCACATTCAGCTTCAAGATGTTACCA 1168 |
| | |
| DB | 200 NNN 259 |
| QY | 1169 GCTGGACTACTGATCGGGAATTCAGACAGCTGATAACAAATATGCATCACCA 1228 |
| | |
| DB | 260 NNN 319 |
| QY | 1229 CCAAGTCAAGATCAATAGTGATGAACAAGAGTAAACAAGAAATATCATC 1288 |
| | |
| DB | 320 NNN 379 |
| QY | 1289 TGACAAGATTCTGCTGCTGGCACTTTCATCATCTGCTGTTGTGGAAAGTG 1348 |
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| DB | 380 NNN 439 |
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[illegible]

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Run on: December 4, 2005, 21:28:08 ; Search time 10016 Seconds
(without alignments)

5141.790 Million cell updates/sec

Title: US-10-792-307-4

Perfect score: 906
Sequence: 1 MSQVKGKLEKRGVGRV.....PSQTHPWSASGKSACRPPH 906

Scoring table:
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Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Word size: 70

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -Fgapop=6
-Fgapext=7 -Ygapop=60 -Ygapext=60 -DELOP=6 -DELEXT=7

Database :

GenEmbl1:
1: gb_da:
2: gb_in:
3: gb_env:
4: gb_on:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pr:
9: gb_ro:
10: gb_sts:

11: gb_sy:
12: gb_un:
13: gb_vl:
14: gb_hcg:
15: gb_pl:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description |
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| 1 | 906 | 100.0 | 3169 | 8 | AF417580 | AF417580 Homo sapi |
| 2 | 198 | 21.9 | 2560 | 6 | AX833218 | AX833218 Sequence |
| 3 | 198 | 21.9 | 2560 | 8 | AK094789 | AK094789 Homo sapi |
| 4 | 102 | 11.3 | 3566 | 6 | CQ850588 | CQ850588 Sequence |
| 5 | 102 | 11.3 | 3566 | 8 | AK127751 | AK127751 Homo sapi |
| 6 | 99 | 10.9 | 884 | 6 | CQ728483 | CQ728483 Sequence |
| 7 | 99 | 10.9 | 3216 | 9 | AF417581 | AF417581 Mus muscu |
| 8 | 95 | 10.5 | 159272 | 8 | HSDJ686C3 | AL049712 Human DNA |
| 9 | 79 | 8.7 | 245113 | 14 | AC156927 | AC156927 Bos tauru |

ALIGNMENTS

| | | | | | |
|------------|---|-------------|------|--------|-----------------|
| RESULT 1 | AF417580 | 3169 bp | mRNA | linear | PRI 05-MAR-2003 |
| LOCUS | AF417580 | | | | |
| DEFINITION | Homo sapiens transmembrane channel-like protein 2 (TM2C) mRNA, complete cds. | | | | |
| ACCESSION | AF417580 | | | | |
| VERSION | AF417580.2 | GI:28642834 | | | |
| KEYWORDS | | | | | |
| SOURCE | | | | | |
| ORGANISM | Homo sapiens | | | | |
| | Homo sapiens (human) | | | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catearrhini; Homiidae; Homo. | | | | |
| REFERENCE | 1 (bases 1 to 3169) | | | | |
| AUTHORS | Kurima, K., Peters, L.M., Yang, Y., Riazuddin, S., Ahmed, Z.M., Naz, S., Arnaud, D., Drury, S., Mo, J., Makishima, T., Ghosh, M., Menon, P.S.N., Deshmukh, D., Oddoux, C., Osterer, H., Khan, S., Riazuddin, S., Deininger, P.L., Hampton, L.L., Sullivan, S.L., Sullivan, J.F., Keats, B.J.B., Wilcox, E.R., Friedman, T.B. and Griffith, A.J. | | | | |
| | Dominant and recessive deafness caused by mutations of a novel gene, TM2C1, required for cochlear hair-cell function | | | | |
| | Nat. Genet. 30 (3), 277-284 (2002) | | | | |
| TITLE | JOURNAL | | | | |
| | PUBMED | | | | |
| | 2 (bases 1 to 3169) | | | | |
| REFERENCE | Kurima, K., Griffith, A.J. and Friedman, T.B. | | | | |
| AUTHORS | Direct Submission | | | | |
| TITLE | Submitted (10-SEP-2001) NIDCD, NIH, 5 Research Court, #2A02, Rockville, MD 20850, USA | | | | |
| JOURNAL | 3 (bases 1 to 3169) | | | | |
| REFERENCE | | | | | |

AUTHORS Kurima, K., Griffith, A.J. and Friedman, T.B.
TITLE Direct Submission
JOURNAL Submitted (03-MAR-2003) NIDDD, NIH, 5 Research Court, #2A02,
Rockville, MD 20850, USA
REMARK Sequence update by submitter
COMMENT On Mar 3, 2003 this sequence version replaced gi:19223982.
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ORIGIN

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Query Match: 100.00% Indels: 0
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US-10-792-307-4 (1-906) x AF417580 (1-3169)

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Db 1876 GAGGTGGATTTCTCTCATGTGTGATTTGATTTAGGAAATGTGCTGGTTGATC 1935
QY 641 PheAnGlnGlyMet11eTrpMetGlySerPheTyrA1A1eProGlyLeuVal1Gly11eAn 660
| | | | |
Db 1936 TTCAAACAAAGAAATGATCTGATGGGCTCCTGTATGCTCCAGGCGCTGGTGGGATTAAT 1995
QY 661 ValLeuArgLeuLeuThrSerMetTyrPheGlnCystrpA1A1eMetSerSerAnVal 680
| | | | |
Db 1996 GTGCTGGCGCTGCTGACCTCATGTACTTCAGTGTGGGGGTGATGAGCAGCAACGT 2055
QY 681 ProH1sGluArgValPheLysA1A1eSerArgSerAnAnPheTyrMetGlyLeuLeuLeu 700
| | | | |
Db 2056 CCCCATGACGGGTGCTCAAGGCTCCCGATCCACACATTTCTAATGGGCTCTGCTG 2115
QY 701 LeuVal1LeuPheLeuSerLeuLeuProVal1A1eTyrThr11eMetSerLeuProSer 720
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Db 2116 CTGGTGTCTTCCTCAAGCTCCGTGGGGGTGCTACACATCATGTCCCTCCACCTCC 2175
QY 721 PheAspCyGlyProPheSerGlyLysAnArgMetTyrAspVal1LeuGlnGluThr11e 740
| | | | |
Db 2176 TTGACGTGGGGCGCTTCACTGGGAAAAAGAAATGTACGATGCTCTCCAAAGAACATTT 2235
QY 741 GluAnAspPheProThrPheLeuGlyLys11ePheA1A1ePheLeuA1A1eAnProGlyLeu 760
| | | | |
Db 2236 GAAAAACAATTTCCCAACCTTCTGGGCAAGATCTTGTCTTCTCCCAATCCAGGCTG 2295
QY 761 11e11eProA1A1eLeuLeuMetPheLeuA1A1eTyrTyrLeuAnSerValSerLys 780
| | | | |
Db 2296 ATCATCCAGGCATCGTGTGATGTCTTGCCCATTTACTACCTGAACCTCAGTTTCAAA 2355
QY 781 SerLeuSerArgA1A1eAnA1A1eGlnLeuArgLysLys11eGlnVal1LeuArgGluValGlu 800
| | | | |
Db 2356 ACCCTTTCGGAGCTAATGCCAGCTGAGGAAAGAAATCCAAATGCTCCGTGAAGTTGAG 2415
QY 801 LysSerH1sLysSerValLysGlyLysA1A1eThrA1A1eArgAspSerGlyLysThrProLys 820
| | | | |
Db 2416 AAGATCACAAAATCTGTAAGGCAAGCCACAGCAGGATTCAGAGGACACACTAA 2475
QY 821 SerSerSerLysAsnA1A1eThrGlnLeuGlnLeuThrLysGluGluThrThrProSer 840
| | | | |
Db 2476 ACAGAGCTCCAAAATGCCACCACTCCAACTCACAAAGAAAGACACTCCCTCT 2535
QY 841 AlaSerGlnSerGlnA1A1eMetAspLysLysA1A1eGlnGlyProGlyThrSerAnSerA1A1e 860
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Db 2536 GCCAGCCAAAGCAAGGCATGACAAAGAGGCGAGGCGCTGGAGCTCCAAATCTGGC 2595
QY 861 SerArgThrThrLeuProA1A1eSerGlyH1sLeuPro11eSerArgProProGly11eGly 880
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Db 2596 AACAAGACACACAGCTGCTGCTGTGACACTTCTAATCTGGGCGCTCGAATCGGA 2655
QY 881 ProAspSerGlyH1sA1A1eProSerGlnThrH1sProTrpArgSerA1A1eSerGlyLysSer 900
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Db 2656 CCAAGATTCTGGACACCCCATCTCAGACTCATCCGTGGAAGTCAAGCTCTGGAAAGAGT 2715
QY 901 AAGlnArpProPhis 906
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Db 2716 GCTCAGAGACCTCCCCAC 2733

RESULT 2
AX833218
LOCUS AX833218 2560 bp DNA linear PAT 15-DEC-2003
DEFINITION Sequence 342 from Patent EP1347046.
ACCESSION AX833218
VERSION AX833218.1 GI:39919353
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
AUTHORS
1 Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R., Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahara,K. and Masuko,Y.
TITLE Full-length cDNA sequences
JOURNAL Patent: EP 1347046-A 342 24-SEP-2003;
Research Association for Biotechnology (JP)
FEATURES
source 1. 2560
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 3,76e-172 Length: 2560
Score: 198.00 Matches: 198
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 21.85% Indels: 0
Gaps: 0

US-10-792-307-4 (1-906) x AX833218 (1-2560)

QY 427 ArgPheLeuArGyValLeuAlaAnPheLeuIleIleCyGysLeuCySglYserGlyTyr 446
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Db 2 AGATTCTGTGTCCTGCTGCGCACTTCTCATCTCTGCTGTTGTGGAAGTGGGTAC 61
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QY 447 LeuIleTyPheValValLyArGserGlnGlnPheSerLyMeGlnAnValSerTrr 466
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Db 62 CTCATTTCATTGTGGTTAACCATCTCAGCAATTCTCCAAATGCAAGATGTCAGCTGG 121
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QY 467 TyGluArGAnGluValGluIleValMetSerLeuLeuGlyMeCPheCySProLeu 486
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Db 122 TATGAAGGAATGAGGTAGATCGTGAATGTCCTGCTTGGAAATGTTTGTCCCGCTCG 181
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QY 487 PheGluHrIleAlaLeuGluWanTyrHsPArGTrHrGlyLeuLysTrpGlnLeu 506
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Db 182 TTGAAGCAATGGCTGCCCTGGAAGATTACCACCACCACTGGAAGTGAAGTGGAGCTG 241
QY 507 GlYArGIllePheAlaLeuPheLeuGlyAsnLeuTyTrHrPheLeuValAlaMetAsp 526
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Db 242 GAGGCACTTTTGACATCTTCCGAGGAACCTTACACATTTCTTGGCCCTGATGGAT 301
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QY 527 AspValHlsLeuLyLeuAlaAnGluLurHlleYAsnIlleThHsTrpThrLeu 546
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Db 302 GATGCCACCTCAACATTCCTGAATGAGACAAATAAAGAACATCACTCACTGGACTCG 361
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QY 547 PheAnTyTrPAsnSerSerGlyTrPAsnGluSerValProArProProLeuHsPro 566
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Db 362 TTTAATTTTACAACTCTCTGGTTGGAAGAGAGGTGCCCGACACCCCTGACCTT 421
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QY 567 AlaAspValProArGlySerCySTrpGluThralAlaGlyIlleGluPheArGLeu 586
|||||
Db 422 GCAAGTGGCCCGGGGGTCTTGCTGGAGACAGCTGTGGCAATGAATTCATGAGGCTG 481
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QY 587 ThrValSerPheLeuValThrTyrlleThrIlleLeuLeuGlyAsPheLeuArGala 606
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Db 482 ACGGTGCCGACATCTCTGTAACGTACATCACTCTGCTGGGGGACTTCTTACGGGCT 541
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QY 607 CySPheValArGPheMetAsnTyrcySrrProCySrrPAsnLeuGluAlaGlyPhe 624
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Db 542 TGTTTTGTGGGGTCAAGAACTACTGCTGGTGGGACTTGGAGGCTGGATT 595
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RESULT 3
AK094789
LOCUS AK094789 2560 bp mRNA linear PRI 30-JUN-2004
DEFINITION Homo sapiens cDNA FLJ37470 fis, clone BRAWH2012258.
ACCESSION AK094789
VERSION AK094789.1 GI:21753918
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
AUTHORS
1 Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,T., Sekina,M., Ohtsuka,M., Nishi,T., Shibahara,T., Tanaka,T., Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahara,K., Murakami,K., Yasuda,T., Iwatsunagi,T., WagaTsuna,M., Shiraishi,A., Sudo,H., Hosolai,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T., Kikkawa,U., Omura,Y., Abe,K., Kimihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M., Ninomiya,K., Ichiishi,T., Yamashita,H., Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hirooka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S., Yoshida,M., Hotsu,T., Kusano,J., Kanohiri,K., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiyasu,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Imose,N., Mutsaers,K., Yuuki,H., Oshima,A., Sasaki,N., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ichihara,T., Shiohara,N., Sano,S., Moriya,S., Nomiyama,H., Satch,N., Takami,S., Tereshima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T.,

RESULT 4
CQ850588
LOCUS CQ850588 3566 bp DNA linear PAT 23-AUG-2004
DEFINITION Sequence 1057 from Patent EPI447413.
ACCESSION CQ850588
VERSION CQ850588.1 GI:51508800
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .3566
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 2.11e-83 Length: 3566
Score: 102.00 Matches: 102
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 11.26% Indels: 0
DB: 6 Gaps: 0
US-10-792-307-4 (1-906) x CQ850588 (1-3566)
QY 625 ProseTyrAlaGluPheAspIleSerGlyAsnValLeuGlyLeuIlePheAsnGly 644
Db 163 CCTCATATGCTAGATTGATATTAGTGAATGTGCTGGTTGATCTTCACACAGGA 222
QY 645 MetIleTpeMetGlySerPheTyrAlaProGlyLeuValGlyIleAsnValLeuArgLeu 664
Db 223 ATGATCTGATGGGCTCCTCTATGCTCCAGGCTGGTGGGCAATTATGTCGGGCTG 282
QY 665 LeuTrSerMetTyrPheGlnCysTrpAlaValMetSerSerAsnValProHisGluArg 684
Db 283 CTGACCTCCATGTACTTCAGTGGCGGTGATGAGCAGCAAGTACCCCATGAACGC 342
QY 685 ValPheValAserArgSerAsnAsnPheTyrMetGlyLeuLeuLeuValLeuPhe 704
Db 343 GTTTCAAAGCTCCCGATCCAGACCACTTCAATGGGCTCTGCTGGTGGTCTTC 402
QY 705 LeuSerLeuLeuProValAlaTyrThrIleMetSerLeuProProSerPheAspCysGly 724
Db 403 CTCACCTCCTGCCGGGTGGCTACACCATCATGTCCTCCACCCCTCTTGACTGGGG 462
QY 725 ProPhe 726
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Db 463 CCGTTC 468
RESULT 5
AK127751
LOCUS AK127751 3566 bp mRNA linear PRI 19-FEB-2004
DEFINITION Homo sapiens cDNA FLJ45851 fls, clone OCBF2018229.
ACCESSION AK127751
VERSION AK127751.1 GI:34534796
KEYWORDS oligo capping; fls (full insert sequence).
SOURCE
ORGANISM Homo sapiens (human)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .3566
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="OCBF2018229"
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223. .711
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SRSNFVWGLLLVLSLLPVAVTINSLPSTDCGPFRCNVSVAEHLPSRGLLRG
PAPRIPLVSCQPVKGHGTLGESPMVFKRVFQDDNVSFCVCAVFFSHQPVAVEC
LK"

ORIGIN

Alignment Scores:
Pred. No.: 2.11e-83 Length: 3566
Score: 102.00 Matches: 102
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 11.26% Indels: 0
DB: 8 Gaps: 0

US-10-792-307-4 (1-906) x AK127751 (1-3566)

QY 625 ProSerTyrAlaGluPheAspIleSerGlyAsnValLeuGlyLeuIlePheAsnGlnGly 644
DB 163 CCTTCATATGCTGAGTTGATATTAGGAAATGCTGGGTTGATCTTCAACCAAGGA 222
QY 645 MetIleTyrMetGlySerPheTyrAlaProGlyLeuValGlyIleAsnValLeuArgLeu 664
DB 223 ATGATCTGATGGGCTCCTCTATGCTCCAGGCTGGTGGCATTAATGCTGGGCTG 282
QY 665 LeuThrSerMetTyrPheGlnCysTrrPalaValIleSerSerAsnValProHisGluArg 684
DB 283 CTGACCTCATGTACTTCAGTCTGCTGGCGCTGATGAGCAAGCAATGCCATGAAGGC 342
QY 685 ValPheValAserArgSerAsnAsnPheTyrMetGlyLeuLeuLeuValLeuPhe 704
DB 343 GTCTCAAAAGCTCCGATCCAACTTCTACATGGGCTCTGCTGCTGGTCTTC 402
QY 705 LeuSerLeuLeuProValAlaTyrThrIleMetSerLeuProProSerPheAspCysGly 724
DB 403 CTCAGCTCCTGCCGGTGGCTACACCATCATGTCCTCCACCTCTTGACTGGGG 462
QY 725 ProPhe 726
DB 463 CCGTTC 468

RESULT 6
LOCUS CQ728483 884 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 14417 from Patent WO02068579.
ACCESSION CQ728483
VERSION CQ728483.1 GI:42297418
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
AUTHORS Venter, C.J., Adams, M.C., Li, P.W., and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humaneons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 14417 06-SEP-2002;

PE Corporation (NY) (US)
Location/Qualifiers
1. 884
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/mol_type="unassigned DNA"
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ORIGIN

Alignment Scores:
Pred. No.: 4.1e-81 Length: 884
Score: 99.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.93% Indels: 0
DB: 6 Gaps: 0

US-10-792-307-4 (1-906) x CQ728483 (1-884)

QY 311 GluGlyTyrIleValTyrSerAlaLeuPheTyrGlyTyrTyrAsnAsnGlnArgThrIle 330
DB 187 GAGGCTATATCAAGTACTCTGCACTTCTATGGCTACTACAAACAAGGACCATC 246
QY 331 GlyTrrPheLeuArgTyrArgLeuProMetAlaTyrPheMetValGlyValSerValPheGly 350
DB 247 GGGTGGCTGAGGACCGAGCTGCTATGGCTTACTTATGGGGGTCAGCGCTGGC 306
QY 351 TyrSerLeuIleIleValIleArgSerMetAlaSerAsnThrGlnGlySerThrGlyGlu 370
DB 307 TACAGCTGATATTGTGATTCATGATGCATGCCAGCATACCAAGAACGACGGGAA 366
QY 371 GlyIleSerAspAsnPheThrPheSerPheValMetPheThrSerTrrPaspTrrLeuIle 390
DB 367 GGGGAGGTGACACTTCACATTCACTTCAGATGTTCAACAAGTGGGACTGACTGATC 426
QY 391 GlyAsnSerGluThrAlaAspAsnValTyrAlaSerIleThrThrSerPheValGlu 409
DB 427 GGGATTCAAGACAGCTGATACAAATATCATCCATCAACACACAGCTTCAAGGA 483

RESULT 7
LOCUS AF417581 3216 bp mRNA linear ROD 05-MAR-2003
DEFINITION Mus musculus transmembrane channel-like protein 2 (Tmc2) mRNA,
complete cds.
ACCESSION AF417581
VERSION AF417581.1 GI:19223984
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Mus.
REFERENCE
AUTHORS Kurama, K., Peters, L.M., Yang, Y., Riazuddin, S., Ahmed, Z.W., Naz, S.,
Arnold, D., Drury, S., Mo, J., Makishima, T., Ghosh, M., Memon, P.S.N.,
Desimukh, D., Odell, C., Oster, H., Khan, S., Riazuddin, S.,
Deininger, P.L., Hampton, L.W., Sullivan, S.L., Bectey, D.F.,
Keats, B.J.B., Wilcox, E.R., Friedman, T.B., and Griffith, A.J.

TITLE Dominant and recessive deafness caused by mutations of a novel gene, TMCI, required for cochlear hair-cell function

JOURNAL Nat. Genet. 30 (3), 277-284 (2002)

PUBMED 11850618

REFERENCE 2 (bases 1 to 3216)

AUTHORS Kurama, K., Griffith, A.J. and Friedman, T.B.

TITLE Direct Submission

JOURNAL Submitted (10-SEP-2001) NIDCD, NIH, 5 Research Court, #2A02, Rockville, MD 20850, USA

FEATURES

source 1..3216

Location/Qualifiers

1..3216

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ORIGIN

Alignment Scores:

Pred. No.: 1,14e-80 Length: 3216

Score: 99.00 Matches: 140

Percent Similarity: 98.59% Conserved: 0

Best Local Similarity: 98.59% Mismatches: 1

Query Match: 10.93% Indels: 2

DB: 9 Gaps: 0

US-10-792-307-4 (1-906) x AF417581 (1-3216)

QY 213 MetAlaLysLysTrpValLysPheLysArgAspPheAspAsnPheLysThrGlnCysAla 232

Db 904 ATGGCTAAGAAATGGGTCAAGTTTAAGAGGAGCTTGATTAATTTTCAAGCTCAATGATTT 963

QY 233 ProTProGluWeLysLysLysAspLLeuGlnSerHisPheGlySerSerValAlaSerTyr 252

Db 964 CCCTGGAGAAATGAATCAAGACATTGAAGTCACTGGCTTCTGTGGCATCTTAC 1023

QY 253 PheIlePheLeuArgTrpMetTyrGlyValAsnLeuValLeuPheGlyLeuIlePheGly 272

Db 1024 TTCATCTTCTCCCATGGATGATGAGATTAACCTGTCTCTTTTGGCTTAATTTGGT 1083

QY 273 LeuValIleIlePheGluValLeuWeLysLysPheProTyrGlySerIleProArgLysThr 292

Db 1084 CTACATCATCATCCCAAGAGTGTCTGATGGGCATGCCCTATGCAAGTATACCCAGAAACAC 1143

QY 293 ValProArgAlaGluGluGlyLysAlaMetAspPheSerValLeuTrpAspPheGluGlu 312

Db 1144 GTGCCTGACCTGAGAGAGAGGCCACCATGACCTCTGTCTGTGGCATTTTGAGGG 1202

QY 312 YTrIleLysTyrSerAlaLeuPheTyrGlyTyrTyrAsnAsnGlnArgThrIleGlyTyr 332

Db 1203 CTACATCAAAATATCTGCTCTCTCTATGGCTACAAACAACAGGAGGATGGATG 1262

QY 332 PleuArgTyrArgLeuProWeLValTyrPheMetValGlyValSerValPheGlyTyrSe 352

Db 1263 GCTGAGGTACAGGCTGCCCATGGCTTACTTATGTGGGGGTCAGGGTGTTGGCTACAG 1322

QY 352 rLeu 353

Db 1323 CTTG 1326

RESULT 8

LOCUS HSDJ6863/c 159272 bp. DNA linear PRI 18-MAY-2005

DEFINITION Human DNA sequence from clone R4-6863 on chromosome 20 contains the IDH3B gene for isocitrate dehydrogenase 3 (NAD+) beta, the NOL5A gene for nucleolar protein 5A (56kDa with KKE/D repeat), the TM2 gene for transmembrane cochlear expressed protein 2, a novel gene, the RNUS6 gene for small nuclear RNA US6, the RNUS7 gene for small nuclear RNA US7, the 5' end of one variant of the ZNF343 gene for zinc finger protein 343 and three CpG islands, complete sequence.

ACCESSION AL049712

VERSION AL049712.12 GI:5629919

KEYWORDS HTG; C20orf145; CpG island; FLJ37470; IDH3B; isocitrate dehydrogenase 3; NOL5A; NOP56; nucleolar protein 5A; RNUS6; RNUS7; small nuclear RNA; TM2; ZNF343.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 159272)

AUTHORS Smith, M.

TITLE Direct Submission

JOURNAL Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: veg@sanger.ac.uk

COMMENT On Jul 28, 1999 this sequence version replaced gi:578962. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Swi, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information

on the WormPeP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep. This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr20>. RP4-666C3 is from the library R1C1-4 constructed by the group of Jong. For further details see <http://www.chori.org/beepec/home.htm>. VECTOR: pCIPAC2.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest except on the rare occasion of the clone being a YAC.

SOURCE

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mRNA

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mRNA

mRNA

9. **গণনা**

mRNA

gene

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BQ367227"

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Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Deville, M. L., Davis, C., Davy-Carroll, L., De Andrade, C., Dedetich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabriel, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gbregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaretna, P., Healand, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladik, S. L., Hodgson, A., Hogue, M., Hollins, B., Howells, S., Huliyil, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jollivet, A., Karpach, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowls, C., Kref, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lornashewa, L., Louisa, H., Lozano, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindratne, M., Mahmood, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., McWhinney, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Mlosoavlevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nsokele, O., Okunnu, G., Olufunso, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Popper, F., Polidexter, A., Popovic, D., Primus, E., Pu, L., Pu, L., Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Rellily, B., Rellily, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivera, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Saverly, G., Scherer, S., Scott, G., Shattam, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smaj, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorrell, R., Soze, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umani, K., Velas, R., Vera, V., Villaana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlaczek, R., Woodard, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G., and Gibbs, R. A.

Direct Submission
Unpublished
2 (bases 1 to 245113)
Worley, K. C.
Direct Submission
Submitted (05-FEB-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 245113)
Baylor Genome Sequencing Consortium.
Direct Submission
Submitted (01-JUL-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 28, 2005 this sequence version replaced gi:58652284.
The sequence in this assembly is a combination of BAC based reads

and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/atl/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: FCNL
Center clone name: CH240-6123
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 231266 bases at least Q40
Consensus quality: 234595 bases at least Q30
Consensus quality: 237389 bases at least Q20
Estimated insert size: 234838; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a "working draft" sequence. It currently
* consists of 29 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 16141: contig of 16141 bp in length
* 16142 16247: gap of 106 bp
* 16248 19049: contig of 2802 bp in length
* 19050 19099: gap of 50 bp
* 19100 37983: contig of 18884 bp in length
* 37984 38499: gap of 516 bp
* 38500 43617: contig of 5118 bp in length
* 43618 43667: gap of 50 bp
* 43668 47955: contig of 4288 bp in length
* 47956 48055: gap of unknown length
* 48056 52532: contig of 4477 bp in length
* 52533 53533: gap of 1001 bp
* 53534 55191: contig of 1658 bp in length
* 55192 55291: gap of unknown length
* 55292 75529: contig of 20238 bp in length
* 75530 76331: gap of 802 bp
* 76332 100155: contig of 23824 bp in length
* 100156 100689: gap of 534 bp
* 100690 120297: contig of 19608 bp in length
* 120298 120347: gap of 50 bp


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* 120346 132375: contig of 12028 bp in length
* 132376 132425: gap of 50 bp
* 132426 136897: contig of 4472 bp in length
* 136898 136947: gap of 50 bp
* 136948 138345: contig of 1398 bp in length
* 138346 138395: gap of 50 bp
* 138396 153574: contig of 15179 bp in length
* 153575 153625 170313: contig of 16689 bp in length
* 153625 170314 170363: gap of 50 bp
* 170364 172270: contig of 1907 bp in length
* 172271 172320: gap of 50 bp
* 172321 183413: contig of 11093 bp in length
* 183414 183463: gap of 50 bp
* 183464 185804: contig of 2341 bp in length
* 185805 185854: gap of 50 bp
* 185855 189662: contig of 4108 bp in length
* 189663 190012: gap of 50 bp
* 190013 192069: contig of 2057 bp in length
* 192070 192119: gap of 50 bp
* 192120 207009: contig of 14890 bp in length
* 207010 207109: gap of unknown length
* 207110 208199: contig of 1090 bp in length
* 208200 208299: gap of unknown length
* 208300 209314: gap of 1015 bp in length
* 209315 209414: gap of unknown length
* 209415 210544: contig of 1130 bp in length
* 210545 210644: gap of unknown length
* 210645 211955: contig of 1311 bp in length
* 211956 212055: gap of unknown length
* 212056 213144: contig of 1089 bp in length
* 213145 213244: gap of unknown length
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* 214653 214752: gap of unknown length
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FEATURES
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gap 120298. 120347
/estimated_length=50
gap 132376. 132425
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gap 136898. 136947

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Alignment Scores:

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|------------------------|----------|---------------|--------|
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| Score: | 79.00 | Matches: | 79 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 8.72% | Indels: | 0 |
| DB: | 14 | Gaps: | 0 |

US-10-792-307-4 (1-906) x AC156927 (1-245113)

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Db 178527 ATGGGTTCTTCTACGGCCCGGACTGGTGGCATTAAATGGTGGCGCTGTGACTCC

178468

QY 668 MetTyrPheGlnCysTfPAlaValMetSerSerAsnValProHsGluArgValPheIys 687

Db 178467 ATGTACTTCAGTGGTGGGAGTGTATGAGCAGCACTCCGCCACGACCGGTGTTCAAG

178408

QY 688 AlaSerArgSerAsnAsnPheTyrMetClyLeuLeuLeuValLeuPheLeuSerIleu 707

Db 178407 GCGTCCGGCTCCACACACTTCTACATGGGGCTCTGCTGGTGGTCTTCTCAGGCTC

178348

QY 708 LeuProValAlaTyrThrIleMetSerLeuProProSerPheAspCysGlyProPhe 726

Db 178347 CTGCCCGTGGCTACACACATCATGCCCTTCCGCCCTCCTTCAGCTGGGGGCAATTC 178291

Search completed: December 5, 2005, 02:29:59
Job time : 10235 secs

XX An isolated or purified nucleic acid molecule encoding transducin-1 (TDC1), TDC2, or its fragment, useful for prognosticating, treating or PT monitoring hearing loss.

XX Claim 9; Fig 2; 85pp; English.

XX The present sequence encodes human transducin-2 (TDC2). The present CC invention describes human and mouse TDC1 and TDC2. Also described: (1) a CC method for detecting hearing loss or predisposition to hearing loss in an CC animal; (2) a method for determining the level of nucleic acid comprising CC wild-type TDC1 or TDC2 gene and/or mutant TDC1 or TDC2 gene in a test CC sample comprising a nucleic acid comprising the wild-type TDC1 or TDC2 CC gene and/or mutant TDC1 or TDC2 gene obtained from the animal; (3) a CC method for detecting the level of wild-type TDC1 or TDC2, and/or mutant CC TDC1 or TDC2 in a test sample comprising a protein comprising the wild- CC type TDC1 or TDC2 gene and/or mutant TDC1 or TDC2 gene in a test sample CC comprising a nucleic acid comprising the wild-type TDC1 or TDC2 gene CC and/or mutant TDC1 or TDC2 gene obtained from the animal; (4) a method CC for treating an animal prophylactically or therapeutically for hearing CC loss due to a complete or partial loss of wild type TDC1 or TDC2; and (5) CC a method for identifying one or more agents that interact with a TDC1 CC and/or TDC2 genes in a cell by administering one or more agents to the CC cell comprising the genes and assaying the expression level of the genes CC by the cell, where an increase or decrease in the expression level is CC indicative of the interaction between the agents and the genes in the CC cell. TDC1 and TDC2 have auditory activities and can be used in gene CC therapy. The molecules, compositions and methods of the present invention CC can be used for prognosticating, treating and monitoring hearing loss

XX Sequence 3121 BP; 778 A; 823 C; 824 G; 696 T; 0 U; 0 Other;

Alignment Scores:

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Score: 879.00 Matches: 879
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.02% Indels: 0
DB: 8 Gaps: 0

US-10-792-307-4 (1-906) x ACC69614 (1-3121)

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QY 48 G1YArGArGLyAlaGLnArGSeRGLnLyGLuArGLaGLyGLySeRProSeRProGLy 67
Db 109 GCGAGGCGCGAGCTCAAGCAAGCAAGAGCGCGCGGGGGGACCCCAAGCCCGGG 168
QY 68 SerProArGLyAGlnThrGLyArGArGhiArGGLuGLuLeuGLyGLuGLnGlu 87
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QY 88 ArGGLyGLuAlaGLuArGLnThrCyGLuGLyArGArGLyArGLyArGLyAlaSeRPho 107
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QY 108 GlnGLuArGLnThrAlaLeProLyArGLyGLyGLuLeProArGLyGLuGLySeR 127
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QY 128 LyArGLnLyLyArProArGSeSerSeSerLeuAlaSeSerAlaSeRGLyGLyUSeR 147
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QY 148 LeuSerGLuGLuGLuAlaGLnLeuGLuGLnValGLuGLyGLyGLyGLyLeuLe 167
Db 409 CTGTCCAGAGAGAAAGTGGCCAGATCTGGAGAGAGTGGAGAGAGAGAGAGCTATT 468

QY 168 AlaThrPhoArGSeRLyProTrpProMetAlaLyLyLeuThrGLuLeuArGLuAla 187
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QY 188 GlnGLuPhoValGLyGLyTrGLuGLyAlaLeuGLyGLyGLyGLyGLyGLnLeuTr 207
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QY 208 AlaTrLySeMetLeuMetAlaLyLyTrValLyPhoLyArGLyArGLyArGLyArGLy 227
Db 589 GCTTACAAAGTCTGATGGCCAGAAATGGGTCAAAATTAAGAGAGACTTGAATATTC 648

QY 228 LyTrGLnCyAlaProTrpGLuLeuLyLyLyAspLyLeuGLySeRHisPhoGLySeR 247
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QY 248 SerValAlaSerTrpPheLeuArGLnTrpMetLyTrGLyValAlaLeuValLeuPhe 267
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 AC AAS92296;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #2100.
 XX

KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Dmanee RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG28109.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XT Claim 1; SEQ ID NO 28100; 103bp; English.
PS
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pat_sequences
XX
SQ Sequence 5027 BP; 1316 A; 1289 G; 1339 G; 1083 T; 0 U; 0 Other;

Alignment Scores:
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Best Local Similarity: 100.00% Mismatches: 0

Query Match: 64.35% Indels: 0
DB: 5 Gaps: 0
US-10-792-307-4 (1-906) * AAS92296 (1-5027)
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|||||
DB 1156 TGCGTAGAGTACCGGCTGCTATGGCTTACTTATGTGGGGGTCAAGCTGTTCGCTAC 1215
QY 352 SerLeuIIeIValIIeArSerMeAlaSerAanThrInGLYSerThrGLYGLY 371
|||||
DB 1216 AGCGTAGATTTGTTCATTCGATGATGGCCAGCAATACCAAGAGGACACGGCGAAGG 1275
QY 372 GLUSeArAaPhaPhetThrPheSerPheLYMePheThrSerTrpAaTYrLeuIIeGLY 391
|||||
DB 1276 GAGAGTGAACAATTCACTTCAAGCTTCAAGATTGTTCAACAGCTGGAGTACTGATCGGG 1335
QY 392 AAnSerGLUThrAlaAaPhaAnLYsTYrAlaSerIIeThrThrSerPheLYGLUSeIIe 411
|||||
DB 1336 AATTCAAGACAGACGTGATTAACAAATATGATCCATCAACAGCTTCAAGAAATCAATA 1395
QY 412 ValAaPGLnGLNGLUSeArAanLYsGLNGLUAnIIeHISLeuThrArGPheLeuArGVal 431
|||||
DB 1396 GTGGATGAACAAGAGAGTAACAAAGAAATATCATCTGACAGATTCTTCGTGTC 1455
QY 432 LeuAlaAnPhaLeuIIeIIeCYsCYsLeuCYsGLYSerGLYrLeuIIeTYrPheVal 451
|||||
DB 1456 CTGGCAACTTCTCATCATCTGCTGTTGTGGAAAGTGGTACTCACTTACTTTGG 1515
QY 452 ValLYsArGSeGLNGLNPhaSerLYsMeGLNAsnValaSerTrPYrGLYArGAnGLY 471
|||||
DB 1516 GTTAAGGATCTCAGCAATCTCCAAATGACAAATGTCAGCTGATGTAAGGAATGAG 1575
QY 472 ValGLUIIeValMeSerLeuLeuGLYMePheCYsProProLeuPhaGLUThrIIeAla 491
|||||
DB 1576 GTAGAGATCGTGAATGCTGCTGTGAATGTTTGTCCCTCTGTTTGAACCATCGCT 1635
QY 492 AlaLeuGLUAnTYrHISProArGThrGLYLeuLYsTrpGLNLeuGLYArgIIePheAla 511
|||||
DB 1636 GCCCTGAGAAATTACCAACCAAGCACTGAGCTGAAGTGGAGCTGGAGCACTTTGCA 1695
QY 512 LeuPhaLeuGLYAsnLeuTYrThrPheLeuLeuAlaLeuMeValaAaPhaValHISLeuLYs 531
|||||
DB 1696 CTCTTCCTGGGGAACCTCTACATTTCTCTGGCCCTGATGATGATCACTCACTCAAG 1755
QY 532 LeuAlaAnGLUGLUThrIIeLYsAanIIeThrHISTrpThrLeuPhaAnTYrTrpAan 551
|||||
DB 1756 CTTCGTATGAAAGACATTAAGAAACATCACTGATGCTGTTTAATATTCAAC 1815
QY 552 SerSerGLYrTrpAanGLUSeArValaProArgProProLeuHISProAlaAaValaProArg 571
|||||
DB 1816 TCTTCTGTGTGAGAGAGAGTGTCCCGAGACACCTGACACCTGAGATGTGCCCGG 1875

QY 572 GAlSerCysTrpGluThrAlaValGlyIleGluPheMetArgLeuThrValSerAspMet 591
 DB 1876 GGTTCTGCTGGGAGACAGCTGGGCATTGAATTCATGAGGCTGACGGTGTCTGACATG 1935
 QY 592 LeuValThrTyrTleThrIleLeuLeuGlyAspPheLeuArgAlaCysPheValArgPhe 611
 DB 1936 CTGGTAACGTACATCAACATCTGCTGGGGAGACTTCAGAGGGCTGTTTGTGGCGTTC 1995
 QY 612 MetAsnTyrCysTrpCysTrpAspLeuGluAlaGlyPheProSerTyrAlaGluPheAsp 631
 DB 1996 ATGAACTAAGTGGTGGTGGAGACTTGAGAGGCTGGATTCTTCATATGCTGAGTTGAT 2055
 QY 632 IleSerGlyAsnValLeuGlyLeuIlePheAsnGlnGlyMetIleTrpMetGlySerPhe 651
 DB 2056 ATTAGGGAAATGCTGGGCTTTCATCTCAACCAAGAGATGATGAGGGCTCCCTTC 2115
 QY 652 TyrAlaProGlyLeuValGlyIleAsnValLeuArgLeuLeuThrSerMetCysPheGln 671
 DB 2116 TATGCTCCAGGCTGGTGGGCAATTAAATGGCTGGGCTGCTCACTCATGTTCTTCAG 2175
 QY 672 CysTrpAlaValMetSerSerAsnValProHISgluArgValPheIysAlaSerArgSer 691
 DB 2176 TGCTGGGGCGGTGATGAGCAGCAAGTACCCCATGACAGCGTGTTCAAAGGCTCCGATCC 2235
 QY 692 AsnAsnPheTyrMetGlyLeuLeuLeuValIleuPheLeuSerIleuLeuProValAla 711
 DB 2236 AACCACTTCTACATGGGCTCTGCTGCTGTGCTCTCTCCAGGCTCCGCGGGTGGCC 2295
 QY 712 TyrThrIleMetSerLeuProProSerPheAspCysGlyProPheSerGlyIysAsnArg 731
 DB 2296 TACCATCATGTCCTCCACGCTCCTTGACTGGCGGCGCTTCAGTGGAGAAAACGAG 2355
 QY 732 MetTyrAspValLeuGlnGluThrIleGluAsnAspPheProThrPheLeuGlyIysIle 751
 DB 2356 ATGTACGATGTCCTCCAAAGAGACCATTTGAAAACGATTCGCAACCTTCGCGGCAAGTC 2415
 QY 752 PheAlaPheLeuAlaAsnProGlyLeuIleIleProAlaIleLeuLeuMetPheLeuAla 771
 DB 2416 TTGGCTTCCCTGGCCAAATCCAGGCTGATCATCCACGCAATCTGCTGATGTTCTGGCC 2475
 QY 772 IleTyrTyrLeuAsnSerValSerIysSerLeuSerArgAlaAsnAlaGlnLeuArgIys 791
 DB 2476 ATTTACTACTGAACTGAACTGAAATCCCTTCGAGAGCTAAATGCCAGCTGAGAGAG 2535
 QY 792 LysIleGlnValLeuArgGluValGluIysSerHisIysSerValIysGlyIysAlaThr 811
 DB 2536 AAATCCAAAGCTCCCTGAACTGAGAAAGATCAAAATCTGTAAGGCAAAAGCCACA 2595
 QY 812 AlaArgAspSerGluAspThrProIysSerSerSerIysAsnAlaThrGlnLeuGlnLeu 831
 DB 2596 GCCAGAGTTCAAGAGACACCTAAACACAGCTCCAAAATGCCACCGCTCCAACTC 2655
 QY 832 ThrIysGluGluThrThrProProSerAlaSerGlnSerGlnAlaMetAspIysIysAla 851
 DB 2656 ACCAAGGAAGACCACTCTCTCCCTCTGCCAGCCAAAGCAAGCCATGACAGAAAGCGC 2715
 QY 852 GlnGlyProGlyThrSerAsnSerAlaSerArgThrThrLeuProAlaSerGlyHisLeu 871

DB 2716 CAGGGCCCTGGACCTCCAAATTCGACAGCAGCAACAGCTGCTGGACACTT 2773
 QY 872 ProIleSerArgProProGlyIleGlyProAspSerGlyHisAlaProSerGlnThrHis 891
 DB 2776 CCTATATCTGGGCCCCCTGGAAATCGAGACGATTCGGCCACGCCCATCTCAACTCAT 2835
 QY 892 ProTrpArg 894
 DB 2836 CCGTCGAGA 2844
 RESULT 3
 ADM01657
 ID ADM01657 standard; cDNA; 2560 BP.
 AC
 XX ADM01657;
 AC
 XX 20-MAY-2004 (first entry)
 DT
 XX
 DE Human cDNA of the invention SEQ ID NO:342.
 PE
 XX
 KW ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.
 OS Homo sapiens.
 XX
 PN EP1347046-A1.
 XX
 PD 24-SEP-2003.
 XX
 PF 12-APR-2002; 2002EP-00008400.
 PE
 XX
 PR 22-MAR-2002; 2002JP-00137785.
 PA
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Negahara K, Masuno Y;
 XX WP1; 2003-723558/69.
 DR P-PSDB; ADM04100.
 DR
 XX
 PT New polynucleotides and polypeptides are useful in gene therapy, for
 PT developing a diagnostic marker or medicines for regulating their
 PT expression and activity, or as a target of gene therapy.
 PS
 XX Claim 1; SEQ ID NO 342; 305bp; English.
 CC
 CC The invention relates to a novel human polynucleotide and the encoded
 CC polypeptide. A polynucleotide of the invention may have a use in gene
 CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
 CC as a primer for synthesizing the polynucleotide or as a probe for
 CC detecting the polynucleotide. The polynucleotides ADM03316-ADM03758 are
 CC useful in gene therapy, for developing a diagnostic marker or medicines
 CC for regulating their expression and activity, or as a target of gene
 CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
 CC are useful as pharmaceutical agents. The present sequence represents a

| | |
|------------------------|-----------|
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| Score: | 198.00 |
| Percent Similarity: | 100.00% |
| Best Local Similarity: | 100.00% |
| Query Match: | 21,853 |
| GB: | 11 |
| Gaps: | 0 |
| Length: | 2560 |
| Matches: | 198 |
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| Mismatches: | 0 |
| Indels: | 0 |
| Gaps: | 0 |

| QY | ABV75613 | standard; cDNA; 2591 BP. | |
|-----|--|---|-----|
| 427 | ATGPhoeLauATgVAlLauLaaanPhoeLauelllAGCySLeuLysG15SerGlyTyr | 446 | |
| 428 | | | |
| 429 | | | |
| 430 | 2 AGATTCTCGTGCTCGTGGCAATCTCTCATCTGCTGTGTGTGGAAAGGGATAC | 61 | |
| QY | 447 | LeuLleTyrPheValValLysatGserGlnGlnPhSerLysGlnGlnValSerTrp | 466 |
| | | | |
| | | | |
| Db | 62 | CTCATTTACTTGTGGTTAAACGATCTGAGCAATCTCCAAATAGCAAGATGCACGTGG | 121 |
| QY | 467 | TyGfLuAAGaGnGluValGluLleValMetSerLeuLeuGlyMetPheCysProPLeu | 486 |
| | | | |
| | | | |
| Db | 122 | TATGAAGAGAAATGAGGTAGAGATCGTAGTCCTCTGGAAATGTTTGTCCCCCTCG | 181 |
| QY | 487 | PhoGluThrIleAlaIleLeuGluAenTyrHisProArgThrGlyLeuLysTTrpGlnLeu | 506 |
| | | | |
| | | | |
| Db | 182 | TTTGAAGAACATCGCTGCGCTGGAGAAATTAACAACCAACGACGTGACTGAAGTGGACGTG | 241 |
| QY | 507 | GlyATGg1lPheAlaIleLeuPheLeuGlyAanLeuTyrThrPheLeuLauLleuMetLAP | 526 |
| | | | |
| Db | 242 | GGACCGATCTTTCGACTCTTCTGGGAACTCTACAACATTTCTTGGCCCTCATGAGAT | 301 |
| QY | 527 | AapValHisIleuLysLeuLalaAnGlnGlnGluThrIleLysAanIleHisTrpThrLeu | 546 |
| | | | |
| Db | 302 | GATGTCCACCTCAAGCTTCTGTAATGAAGAGCAATTAAGAAATCACTCATCGACTCG | 361 |
| QY | 547 | PheAenTyrTyrAanSerSerGlyTrpAanGlnSerValProArgProLeuHisPro | 566 |
| | | | |
| Db | 362 | TTTAACATTTAAACAACCTTCTGGTTGGAACAGAGGTGCTCCGCCACACCCCTGCACCT | 421 |
| QY | 567 | AlaLeaPValProArgGlySerCysTrpGluThrAlaValGlyIleGluPheMetArgLeu | 586 |
| | | | |
| Db | 422 | GCAAGATGTCGCCGGGTCTTCTGTGGAGACAGCTGTGGCAATGAATCATAGAGCTG | 481 |
| QY | 587 | ThrValSerAspMetLeuValThrTyrIleThrIleLeuLeuGlyAspPheLauArgAla | 606 |
| | | | |
| Db | 482 | AACGGTGTCCACATGCTGTGTAAGTACATCAACATCTGTGAGGAGACTTCTTAAGGGCT | 541 |
| QY | 607 | CysPheValArgPheMetAanTyrCysTrpCysTrpAspLeuGlnLalaGlyPhe | 624 |
| | | | |
| Db | 542 | TGTTTGTGGGGTTCATGAACATGCTGCTGCTGGGACTTGAAGCGCTGAAATT | 595 |

| | |
|----|---|
| XX | ABV75613; |
| AC | |
| DT | 23-JAN-2003 (first entry) |
| XX | |
| DE | Human ribosomal protein L3220.9 cDNA. |
| XX | |
| KW | Human; ribosomal protein L3220.9; diabetes; menstrual disorder; anaemia |
| RW | peptic ulcer; arrhythmia; epilepsy; gene; ss. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| FT | Key Location/Qualifiers |
| EH | CDS 74..646 |
| FT | /tag= a |
| FT | /product= "ribosomal protein L3220.9" |
| XX | |
| PN | CN1345827-A. |
| XX | |
| PD | 24-APR-2002. |
| XX | |
| PE | 29-SEP-2000; 2000CN-00125511. |
| XX | |
| ER | 29-SEP-2000; 2000CN-00125511. |
| XX | |
| PA | (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC. |
| PI | Mao Y, Xie Y; |
| XX | |
| DR | WPI: 2002-548952/59. |
| P | P=SDBI; ABP57746. |
| PT | Novel polypeptide-human ribosomal protein L3220.9 and encoding |
| PT | polynucleotide for treating diabetes, menstrual disorder, peptic ulcer, |
| XX | arrhythmia, anemia and epilepsy. |
| PS | Claim 6; Page 25-26 (Disclosure); 33pp; Chinese. |
| XX | |
| CC | The invention relates to the novel human ribosomal protein L3220.9, and |
| CC | the polynucleotide encoding it. The protein is useful for treating |
| CC | diabetes, menstrual disorder, peptic ulcer, arrhythmia, anaemia and |
| CC | epilepsy. Also disclosed is an antagonist for resisting the polypeptide |
| CC | and its therapeutic action, and the application of the polynucleotide. |
| CC | The present sequence encodes the human ribosomal protein L3220.9 of the |
| XX | Invention |
| SQ | Sequence 2591 BP; 576 A; 670 C; 557 G; 788 T; 0 U; 0 Other; |

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 4.67e-136 | Length: | 2591 |
| Score: | 153.00 | Matches: | 153 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 16.89% | Gaps: | 0 |
| DB: | 6 | | |

US-10-792-307-4 (1-906) * ABV75613 (1-2591)

| | | |
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| | XX | 14-FEB-2003; 2003JP-00102207. |
| | PR | 09-MAY-2003; 2003JP-00131452. |
| | XX | (REAS-) RES ASSOC BIOTECHNOLOGY. |
| | PA | |
| | XX | |
| P1 | Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T; | |
| P1 | Makematsu A, Ishii S, Nagai K, Irie R; | |
| XI | | |
| DR | WPI: 2004-583265/57. | |
| DH | P-P5DB; ADM09507. | |
| PT | New 1995 cDNA, useful for treating osteoporosis, neurological diseases, | |
| PT | Alzheimer's diseases, Parkinson's diseases, dementia and various cancers. | |
| XX | | |
| PS | Claim 1; SEQ ID NO 1057, 2686pp; English. | |
| CC | This invention relates to novel, isolated full length human cDNA | |
| CC | molecules and the encoded proteins thereof. Specifically, it refers to | |
| CC | cDNA clones obtained by an oligo-clipping method, where none of these | |
| CC | clones are identical to any known human mRNAs. The present invention | |
| CC | describes an immunoassay to identify agonists and antagonists, as well as | |
| CC | antibodies, antisense molecules and siRNAs that can all be used to bind | |
| CC | to and modulate expression of the cDNA molecules. As such, these | |
| CC | molecules are useful for diagnostic markers or therapeutic targets for | |
| CC | the various diseases or morbid states. In particular, they are useful in | |
| CC | a gene therapy for treating osteoporosis, neurological disease, Alzheimer's | |
| CC | disease, Parkinson's disease, dementia, short memory and various cancers, | |
| CC | as well as for maintaining equilibrium of sense or motor function, and | |
| CC | for treating emotional reaction, fear response and panic. Accordingly, | |
| CC | they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian, | |
| CC | cystostatic and tranquilliser activities. This polynucleotide is a full | |
| CC | length human cDNA sequence of the invention. NOTE: This sequence is not | |
| CC | given in the sequence listing of the specification but can be obtained on | |
| CC | CD-ROM from the European Patent Office, Vienna Sub-office. | |
| XX | | |
| SQ | Sequence 3566 BP: 989 A; 791 C; 877 G; 909 T; 0 U; 0 Other; | |
| Alignment Scores: | | |
| Pred. No.: 5..7e-87 Length: 3566 | | |
| Score: 102.00 Matches: 102 | | |
| Percent Similarity: 100.00% Conservative: 0 | | |
| Best Local Similarity: 100.00% Mismatches: 0 | | |
| Query Match: 11.26% Indels: 0 | | |
| DB: 13 Gaps: 0 | | |
| US-10-792-307-4 (1-906) x ADM07551 (1-3566) | | |
| QY 625 ProserGyrralacglurPheaprlisecrclyAanVallandulyleuiIephdaenongtoly 644 | | |
| Db 163 CCTTCATACCTGAAGATTGTATTAATGGAAATGCGTGCGTTTACTCTCAACAAGA 222 | | |
| QY 645 MetlIerPhetGcySerPherGzrLAPRogLyLeuValGLyl1aaNvaLLaufrAgLeu 664 | | |
| Db 223 ATGATCTGCATGGGCTCCTTCTATCTCCAGAGGCGTGGTGGCATTTAAATGTCTGCCGCTG 282 | | |
| QY 665 LeufthrSertwctyrPheagncyArTralaValtheUcSerAnvalProhiJgLuArg 684 | | |

Db 283 CTGACCTCCATGACTGCTGGGCGGTGATGACGACCAAGTACCCCATGAACGC 342
 QY 685 ValPheValAspSerArgSerAspAspPheTyrMetGlyLeuLeuLeuValLeuPhe 704
 Db 343 GTGTCAAAAGCTCCGATCCAAACAATTCTACATGGGCTCTGCTGCTGGTCTTC 402
 QY 705 LeuSerLeuLeuProValAlaGlyThrIleMetSerLeuProProSerPheAspGly 724
 Db 403 CTCAGCCCTCCTGCCGGTGCGCTACACCATCATGTCCCTCCACCCCTCTTGACTGGCGG 462
 QY 725 ProPhe 726
 Db 463 CCGTTC 468
 RESULT 6
 ACC69616
 ID ACC69616 standard; cDNA; 3216 BP.
 AC ACC69616;
 XX
 DT 18-JUL-2003 (first entry)
 XX
 DE Mouse transductin-2 (TDC2) encoding cDNA SEQ ID NO:7.
 XX
 KW Mouse; transductin-2; TDC2; hearing loss; auditory; gene therapy; gene;
 KW 55.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 322..2988
 FT /*tag= a
 FT /product= "transductin-2"
 XX
 PN W02003025140-A2.
 PD 27-MAR-2003.
 XX
 PF 19-SEP-2002; 2002MO-US029614.
 XX
 PR 19-SEP-2001; 2001US-0323275P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Griffith AJ, Kurima K, Wilcox E, Friedman T;
 XX
 DR WPI: 2003-371806/35.
 DR P-PSDB; ABR43618.
 XX
 PT An isolated or purified nucleic acid molecule encoding transductin-1
 PT (TDC1), TDC2, or its fragment, useful for prognosticating, treating or
 PT monitoring hearing loss.
 XX
 PS Claim 10; Fig 4; 85pp; English.
 CC The present sequence encodes mouse transductin-2 (TDC2). The present

CC invention describes human and mouse TDC1 and TDC2. Also described: (1) a
 CC method for detecting hearing loss or predisposition to hearing loss in an
 CC animal; (2) a method for determining the level of nucleic acid comprising
 CC wild-type TDC1 or TDC2 gene and/or mutant TDC1 or TDC2 gene in a test
 CC sample comprising a nucleic acid comprising the wild-type TDC1 or TDC2
 CC gene and/or mutant TDC1 or TDC2 gene obtained from the animal; (3) a
 CC method for detecting the level of wild-type TDC1 or TDC2, and/or mutant
 CC TDC1 or TDC2 in a test sample comprising a protein comprising the wild-
 CC type TDC1 or TDC2 gene and/or mutant TDC1 or TDC2 gene in a test sample
 CC comprising a nucleic acid comprising the wild-type TDC1 or TDC2 gene
 CC and/or mutant TDC1 or TDC2 gene obtained from the animal; (4) a method
 CC for treating an animal prophylactically or therapeutically for hearing
 CC loss due to a complete or partial loss of wild type TDC1 or TDC2; and (5)
 CC a method for identifying one or more agents that interact with a TDC1
 CC and/or TDC2 genes in a cell by administering one or more agents to the
 CC cell comprising the genes and assaying the expression level of the genes
 CC by the cell, where an increase or decrease in the expression level is
 CC indicative of the interaction between the agents and the genes in the
 CC cell. TDC1 and TDC2 have auditory activities and can be used in gene
 CC therapy. The molecules, compositions and methods of the present invention
 CC can be used for prognosticating, treating and monitoring hearing loss
 XX
 SQ Sequence 3216 BP; 847 A; 808 C; 813 G; 748 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 3,91e-84 Length: 3216
 Score: 99.00 Matches: 140
 Percent Similarity: 98.59% Conservative: 0
 Best Local Similarity: 98.59% Mismatches: 1
 Query Match: 10.93% Indels: 2
 DB: 8 Gaps: 0
 US-10-792-307-4 (1-906) x ACC69616 (1-3216)
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 Db 904 ATGCGTAAGAAATGGGTCAAGATTTAAGAGGAACTTGTAAATTTCAAGACTCAATGTATT 963
 QY 233 ProTTPGluMetIysIleIysAspIleGluSerHisPheGlySerSerValAlaSerTyr 252
 Db 964 CCGTGGAAATGAAATCAAGATCAAGACATTGAAGTCACTTGCTCTTGTGGCACTTAC 1023
 QY 253 PheIlePheLeuArgTTPMetTyrGlyValAsnLeuValLeuPheGlyLeuIlePheGly 272
 Db 1024 TTCAATCTTTCTCCGATGGATGTATGAGATTACCTTGTCTTTGGCTTAATTTGGT 1083
 QY 273 LeuValIleIlePProGluValIleuMetGlyMetProTyrGlySerIlePheArgIysThr 292
 Db 1084 CTAGTCATCATCCGAGAGGCTGCTGATGGCATGCCCTATGGAAGTATACCAAGAAAGACG 1143
 QY 293 ValProArgAlaGluGluGluIys-AlaMetAspPheSerValIleuTPAspPheGluG 312
 Db 1144 GTGCCTGAGACTGAGGAAAGCG-AGCCATGAGACTTCTGTGCTTTGGGATTTTGAGGG 1202
 QY 312 YTrIleIysTyrSerAlaLeuPheTyrGlyTyrIysAsnGlnArgThrIleGlyTyr 332
 Db 1203 CTACATCAATATCTGCTCTCTCTATGAGTACTACAAACACGAGGACCATGTGATG 1262

QY 332 PLeuArgTyrArgLeuProMetAlaTyrPheMetValGlyValSerValPheGlyTyrse 352
 |||
 Db 1263 GCTGAGGTACAGGCTGCCCATGGCTTACTTATGTGGGGGTCAAGCGTGTGGCTACAG 1322
 QY 352 rLeu 353
 |||
 Db 1323 CTTG 1326

Search completed: December 4, 2005, 23:39:31
 Job time : 1147 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 23:18:08 ; Search time 380 Seconds
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 Ygapop 60.0 , Ygapext 60.0
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Word size: 70

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Query | |
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| No matches found | | |

Search completed: December 5, 2005, 04:35:25
Job time : 380 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 23:28:31 ; Search time 1463 Seconds
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5121.023 Million cell updates/sec

Title: US-10-792-307-4
Perfect score: 906
Sequence: 1 MSRYKGLKEARGCKGRV.....PSQTHPWRSASCKAQRPH 906

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Word size: 70

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
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-DB=Published_Applications_NA_Main -QFMT=fastp -SUFFIX=p2noligo.rpbm
-MINMATCH=0.1 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=70
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-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREDS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELDP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*

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| 7: | /cgn2_6/ptodata/1/pubpna/US10C_PUBCONB.seq:* |
| 8: | /cgn2_6/ptodata/1/pubpna/US10D_PUBCONB.seq:* |
| 9: | /cgn2_6/ptodata/1/pubpna/US10E_PUBCONB.seq:* |
| 10: | /cgn2_6/ptodata/1/pubpna/US11_PUBCONB.seq:* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|---------------------|-------------------|
| 1 | 906 | 100.0 | 3169 | 9 | US-10-792-307-3 | Sequence 3, Appl1 |
| 2 | 879 | 97.0 | 3121 | 8 | US-10-487-887-3 | Sequence 3, Appl1 |
| 3 | 583 | 64.3 | 4895 | 6 | US-10-115-831-134 | Sequence 134, App |
| 4 | 583 | 64.3 | 5027 | 9 | US-10-450-763-28100 | Sequence 28100, A |
| 5 | 198 | 21.9 | 2560 | 6 | US-10-108-260A-342 | Sequence 342, App |
| 6 | 99 | 10.9 | 3216 | 8 | US-10-487-887-7 | Sequence 7, Appl1 |
| 7 | 99 | 10.9 | 3216 | 9 | US-10-792-307-7 | Sequence 7, Appl1 |

ALIGNMENTS

RESULT 1
US-10-792-307-3
; Sequence 3, Application US/10792307
; Publication No. US20050196759A1
; GENERAL INFORMATION:
; APPLICANT: Gliffith, Andrew J.
; APPLICANT: Kurima, Kiyoko
; APPLICANT: Wilcox, Edward
; APPLICANT: Friedman, Thomas
; TITLE OF INVENTION: TRANSDUCTIN-1 AND TRANSDUCTIN-2 AND APPLICATIONS TO HEREDITARY
; TITLE OF INVENTION: DEAFNESS
; FILE REFERENCE: 227540
; CURRENT APPLICATION NUMBER: US/10/792,307
; CURRENT FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 3169
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-792-307-3

Alignment Scores:

Pred. No.: 0 Length: 3169
Score: 906.00 Matches: 906
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-10-792-307-4 (1-906) x US-10-792-307-3 (1-3169)

QY 1 MetSerHisGlnValIysGlyLeuIysGluGluValAArgGlyGlyValIysGlyArgVal 20
Db 16 ATGAGCCACCAAGTAAAGCGCTGAAAGAGACACAGAGCGGAGTGAAGAGCGGAGT 75

QY 21 LysSerIysSerProHisThrGlyAspArgLeuGlyAArgArgSerSerIysArgAla 40
Db 76 AAGAGCGGCTCTCCACACAGGTGACAGGCTGGGAAGGACATCTCAAGCAAGCGGCT 135
QY 41 LeuIysAlaGluIYThrProGlyArgArgGlyAlaGlnArgSerGlnIysArgAla 60
Db 136 CTCMAAGCCAGAGGAGCCCAAGGACGGCGGACCTACACCAAGCCAGAGAGCGGCG 195
QY 61 GlyIysSerProIysSerProArgArgLysGlnThrGlyArgArgHisArg 80
Db 196 GGGGCGAGCCCAAGCCCGGGGCTCTCCCGGAGGAGCAAGAGGGGCGAGACAGAA 255
QY 81 GluGluLeuGlyGluGlnGluArgGlyAlaGluArgThrCysGluGlyArgArgLys 100
Db 256 GAAGAGCTGGGGAGCAGAGAGCGGGGCGAGGAGAGAGAGAGAGAGAGAGAGAG 315
QY 101 ArgAspGluArgLysSerPheGlnGluArgThrAlaLeuProIysArgGlyLysGluIle 120
Db 316 CCGAGACAGAGGGGCTCTTCCAGAGCGGACAGCCAGCCCAAGAGGAGAGAGAGATT 375
QY 121 ProArgLysGluGluLysSerLysArgGlnLysLysProArgSerSerSerLeuAlaSer 140
Db 376 CCGAGAAAGAGAGAGAGAGTCAAGCGGCGAGAAAGAGAGAGAGAGAGAGAGAGAG 435
QY 141 SerAlaSerGlyGlyGluSerLeuSerGluGluLeuAlaGlnIleLeuGluGlnVal 160
Db 436 AGTGCTCTGTGGGAGTCCCTGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 495
QY 161 GluGluLysLysLysLeuIleAlaThrMetArgSerLysProThrProMetAlaLysLys 180
Db 496 GAAAGGAGGAG 555
QY 181 LeuThrGluLeuArgGluAlaGlnIlePheValGluLysTyrgluGlyAlaLeuGlyLys 200
Db 556 CTGACAGAGCTCAGGAGAGCCCAAGGATTTGTGAAGAGATGAAGGTGCTGGAAAG 615
QY 201 GlyIysGlyArgGlnLeuTyralaTyrlsMetLeuMetAlaLysLysIrpValLysPhe 220
Db 616 GGAAGAGGAG 675
QY 221 LysArgAspPheAspAsnPheLysThrGlnCysIleProThrGluMetLysIleLysAsp 240
Db 676 AAGAGAGAGCTTGATTAATTCAGAGCTCAATGATTCCTCGGAAATGAAGATCAAGAG 735
QY 241 IleGluSerHisPheGlySerSerValAlaSerTyrrPheIlePheLeuArgTrpMetTyrr 260
Db 736 ATTGAAAGTCACTTGATGCTCTCAGTGGCATCGATTCATCTTCTCCAGATGATAT 795
QY 261 GlyValAsnLeuValLeuPheGlyLeuIlePheGlyLeuValIleIleProGluValLeu 280
Db 796 GAGGTAACTTGCTCTTTGGCTTAATTTGGCTTAATTCAGATCAATCCAGAGATACG 855
QY 281 MetGlyMetProTyrglySerIleProArgLysThrValProArgAlaGluGluLys 300
Db 856 ATGGCATGCTCAATGGAGATATCCAGAAAGACAGTCTCGGCTGAGAAAGAAAG 915
QY 301 AlaMetAspPheSerValLeuTrpAspPheGluGlyTyrlleLysTyrrSerAlaLeuPhe 320

| | | | |
|----|------|---|------|
| Ds | 1735 | ATTGATTTCAATGAGCGGTGTCTGACATCGTGGTAAGTACATCAACATCTCGTGG | 1815 |
| QY | 601 | GLyApHeuLeuAaTgAlAcYsPheValAqPheWeAaSnTyCySrTPCySrTPApLeuA | 620 |
| Ds | 1816 | GGGGACTTCCTACGGGGCTGTGTGTGTCCGGTTCATGAACACTCGTGGTGGGACTGG | 1875 |
| QY | 621 | GLuAlaGLyPheProSerTyAlaGLuPheAplIleSerGLyAanValLeuAlIleA | 640 |
| Ds | 1876 | GAGCGTGGATTCCTCTCATATCTGAATTTGATATATAGTGGAAATGTCGTGGGTTGATC | 1935 |
| QY | 641 | PheAaGLnGLyMetIleTrpHeGLySerPheTyAlaPProGLyLeuAlGLyIleAa | 660 |
| Ds | 1936 | TCACCAACAAGAAATGATCTGAAGGAGCGCTCTTATCTCCAGGCGCTGGTGGGCAATTAAT | 1995 |
| QY | 661 | ValLeuAaTgLeuAaThPheSerHeTyPheGLnCySrPAlaValIleWeSerSerAanVal | 680 |
| Ds | 1996 | GTGTGGCGCTCTGAACCTTCATGACTTCACGTGGTGGGCGGATGATGAGCAACAGTA | 2055 |
| QY | 681 | ProHISGLuArGValPheValAserAqSerAaSnPheTyPheGLyLeuLeuA | 700 |
| Ds | 2056 | CCCATGACAGCGGTGTCAAACCGTCCCATGCAACAACCTCTCATAGGGGCTCTGCTG | 2115 |
| QY | 701 | LeuValLeuPheLeuSerLeuLeuPProValAlaTyTrHISLeuSerLeuPProPProSer | 720 |
| Ds | 2116 | CTGGGTGCTCTCTCTACGCGCTCGCGGTGGCTACACATCATGCTCCCTCCACCTCC | 2175 |
| QY | 721 | PheAaPCCyGLyPProPheSerGLyAaAaArGHeCTTyAaPValLeuGLnGLyThIle | 740 |
| Ds | 2176 | TTTGATCGCGCGCGCTTCAGTGGGAAAGAAACAGATGACATGTCTCCAGAAAGACATT | 2235 |
| QY | 741 | GLuAaAaPhePProThPheLeuGLyAaIlePheAlaPheValAaAaPProGLyAa | 760 |
| Ds | 2236 | GAAGAACATTCACCACTTCCTGGGCAAGATCTTCTGCTTCCTGCGCAATCCAGGCGCTG | 2295 |
| QY | 761 | IleIleTrpAlaIleLeuAaWePheLeuAlaIleTyCTTyLeuAaSerAaSerTyA | 780 |
| Ds | 2296 | ATCATTCACACCACTCGCTGATGTCTCTGGCAATTAACACTGAACATCAAGTTTCCAAA | 2355 |
| QY | 781 | SerLeuSerAaGLaAaAaAaGLnLeuAaTgLyAaIleGLnValaLeuAaTgLyAaGLu | 800 |
| Ds | 2356 | AGCGTTTCCGAGCGAATGCGCACGTGAAGAAAGAAATCCAAAGTGTGCGTGAAGTTGAG | 2415 |
| QY | 801 | LySserHISLySserValLySGLyAaAlaThAlaArGAPSerGLuAaPThPProLyA | 820 |
| Ds | 2416 | AAGAGTCAAAATCTGTAAAGGCAAGCCACCGCAGATTCAGAGGACACCTTAAA | 2475 |
| QY | 821 | SerSerSerGLyAaAaAlaThGLnLeuGLnLeuAaThGLyAaGLuGLyThThPProPProSer | 840 |
| Ds | 2476 | AGGAGCTCCAAAATGCGACCGACGCTCCAACTCCACAAAGAAAGAGACACCTCTCCCTCT | 2535 |
| QY | 841 | AlaAserGLnSerGLnAlaLeuAaPLyAaLyAaGLnGLyProGLyThHISerAaSerAa | 860 |
| Ds | 2536 | GCAACACCAAGGAGCGCATGGACAGAGAGGCGCGGCGCGTGGACATTCGATTCGCC | 2595 |
| QY | 861 | SerArGThThThLeuPProAlaSerGLyHISLeuPProIleSerAaGPProProGLyIleGLy | 880 |
| Ds | 2596 | ACGAGGACCAACATGCTGCTGCTGAGACACTCTCATATCTGCGGCGCCCTGGAATTCGAA | 2655 |

| | | | | | | |
|--|---------|---------------|---|----------|-------------|------|
| OY | | 881 | Prokaryotic | Sequence | US/10487867 | 900 |
| OY | | 881 | Prokaryotic | Sequence | US/10487867 | 900 |
| Db | | 2656 | CCAGATTCGGGCGACGCCCATCTCAGACTCATCCGTGGAGGTCAAGCTTGGAAAGAT | | | 2715 |
| OY | | 901 | AAGlnArGProPheHis | 906 | | |
| Db | | 2716 | GCTCAGAGACTCCCCAC | 2733 | | |
| RESULT 2 | | | | | | |
| US-10-487-887-3 | | | | | | |
| / Sequence 3, Application US/10487867 | | | | | | |
| / Publication No. US20040249139A1 | | | | | | |
| / GENERAL INFORMATION: | | | | | | |
| / APPLICANT: Grifflith, Andrew J | | | | | | |
| / APPLICANT: Kuriyama, Kiyoko | | | | | | |
| / APPLICANT: Wilcox, Edward | | | | | | |
| / APPLICANT: Friedman, Thomas | | | | | | |
| / TITLE OF INVENTION: TRANSDUCTIN-1 AND TRANSDUCTIN-2 AND APPLICATIONS TO HEREDITARY | | | | | | |
| / TITLE OF INVENTION: DEAFNESS | | | | | | |
| / FILE REFERENCE: 226544 | | | | | | |
| / CURRENT FILING DATE: US/10/487,867 | | | | | | |
| / CURRENT FILING DATE: 2004-02-26 | | | | | | |
| / PRIOR APPLICATION NUMBER: PCT/US02/29614 | | | | | | |
| / PRIOR FILING DATE: 2002-09-19 | | | | | | |
| / PRIOR APPLICATION NUMBER: 60/323,275 | | | | | | |
| / PRIOR FILING DATE: 2001-09-19 | | | | | | |
| / NUMBER OF SEQ ID NOS: 8 | | | | | | |
| / SOFTWARE: Patent version 3.2 | | | | | | |
| / SEQ ID NO 3 | | | | | | |
| / LENGTH: 3121 | | | | | | |
| / TYPE: DNA | | | | | | |
| / ORGANISM: Homo sapiens | | | | | | |
| US-10-487-887-3 | | | | | | |
| Alignment Scores: | | | | | | |
| Pred. No.: | 0 | Length: | 3121 | | | |
| Score: | 879.00 | Matches: | 879 | | | |
| Percent Similarity: | 100.00% | Conservative: | 0 | | | |
| Best Local Similarity: | 100.00% | Mismatches: | 0 | | | |
| Query Match: | 97.02% | Indels: | 0 | | | |
| DB: | 8 | Gaps: | 0 | | | |
| US-10-792-307-4 (1-906) x US-10-487-887-3 (1-3121) | | | | | | |
| OY | | 28 | GLAAPARGLUGLYARGRSERSESLYARGLALALEULYLALAGLUGLYHPR | 47 | | |
| Db | | 49 | GGTGACAGCTGGGAAGAGATCTCMAAGAGGGGCTCTCAAAGCGGAGGCCCA | 108 | | |
| OY | | 48 | GLYARGAGGLYALAGlnArSerGlnLYSGlnrGAlaGLYSerProclY | 67 | | |
| Db | | 109 | GGCAGCGCGAGGCTCAGCGAAGCCAGAAGAGCGCGCGGGGAGGCCCAAGCCGGGG | 168 | | |
| OY | | 68 | SERPROARGGLYSGlnThGLYARGARGRHAKRGlUGlUGLUGlUGlUGlUGlU | 87 | | |
| Db | | 169 | TCTCCCGAGAGAAACAGGCGCGAGAGACAACAGAAAGACTGGGGAGAGAGAG | 228 | | |
| OY | | 88 | ARGGLUGLUALAGLUARGTHCYSGlUGLYARGLYVARGASPPGLYARGLSERPHE | 107 | | |
| Db | | 229 | CGGCGGAGGAGAGAGAGACTCGGAGGGCGAGAGAAAACCGAGACGAGGGGCCTCTTC | 288 | | |
| OY | | 108 | GlnGluArgThrAlaAProLYSARGlULysGLULSPoRGLYSGlULYSSer | 127 | | |
| Db | | 289 | CAGGAGCGGACACAGCCCCCMAGGGGAAAAGAGATTCCGAGGAAGAGGAGAGTCC | 348 | | |
| OY | | 128 | LYSARGlULYSLYPRoARGSERSESLYALASERALASERGLYGLUSER | 147 | | |
| Db | | 349 | AAGCGGAGAGAAACCAGGCTCATCTCTGGCTCGAGCTGCTGTTGGGAGGTCC | 408 | | |
| OY | | 148 | LLeuSERGlUGlUGlULeULalAGlnLaleuGLUGlNValGlUGlULYSLYSLeULle | 167 | | |
| Db | | 409 | CTGTCCGAGGAGGAGACTGGCCAGATCCTGGAGGAGGTTGAAAGAAAAAGAAAGCTCAT | 468 | | |
| OY | | 168 | ALAthrHeLrGrSERLYSPROTPrPheGLALYSLYLeUTHrgLLeuArgGLUALe | 187 | | |
| Db | | 469 | GCACCATGGGAGGAGAACCCCTGGCCATGGCGAAAGAACTGACAGAGCTCAGGGAGGCC | 528 | | |
| OY | | 188 | GlnGluPheVALGLULYSLYSGlUGlUALeULYSLYSGlULYSLYSGlnLeUTHr | 207 | | |
| Db | | 529 | CAGGAATTGTGGAGAGATAGAAAGTCCCTGGGAAAGGGGAAAGGCAAGCACTATAT | 588 | | |
| OY | | 208 | ALAThrLYSLShelLeuMeCALALYSLYTrPALYSLYSLYSLYSLYSLYSLYSLYSL | 227 | | |
| Db | | 589 | GCCTACAAAGTCTGATGGCCGAGAAAGGGGTCAATTTTAAGAGAGCTTGATATTTTC | 648 | | |
| OY | | 228 | LYSThrGlnCYslEPROTPrGLueLcYslLELYASPILLEGUsHLshPheGLYSer | 247 | | |
| Db | | 649 | AAGACTCAATGATCCCTCGGGAATAGAAAGTCAAGACATTGAAAGTCACTGGTTCT | 708 | | |
| OY | | 248 | SerVALAsErTYrPhellLePheLauRgrTPheCTYrGLYVALAsnLeuValLeuPhe | 267 | | |
| Db | | 709 | TCAGTGGCATCGATTATTCATCTTCCAGTAGATGTATGAGATTAACCTGCTCTTTT | 768 | | |
| OY | | 268 | GLYLeuLIlePheGLYLeuVALIleIEProCLVALLeuMeGLYHePProTYGLYSer | 287 | | |
| Db | | 769 | GGCTTAATATTGTGTAGTCATTAATCCCAAGAGTACTGATGGCATGCCCTATGGGAGT | 828 | | |
| OY | | 288 | ILEProARGLYSHrVALProARGlAGlUGlUGlULYSLALeHeCaSPheSerValLeu | 307 | | |
| Db | | 829 | ATTCACGAAAGACAGTCCCTCGGGCTGAGGAGAAAGAGCCATGATTTTTCTGTCTT | 888 | | |
| OY | | 308 | TRPLeuPheGLUGlULYTrILELYSYrSERALLeuPheTYrGLYTrYrAsnAsnGln | 327 | | |
| Db | | 889 | TGGGATTTTGAAGGCTATATCAAGTACTGCACTCTCTATGAGTACTACAAACAACAG | 948 | | |
| OY | | 328 | ArgTHRlleGLYTrPLLeuAglTYrARGLeuPheCALATYrPheHeCVALGLYSLer | 347 | | |
| Db | | 949 | AGGACCATCGGGGTGAGATACCGGGCTGCTATGGCTATTATGGTGGGGGTCAAG | 1008 | | |
| | | | | | | |

| | | | |
|----|------|--|------|
| Db | 1309 | ATGGGCTCCCTCTAGTGCACAGCGCTGGTGGGCAATTAAAGTGTGGCGCTGCTGACCTCC | 1968 |
| QY | 668 | MetCysPheGlnCysTrrpAlaValMetSerSerAsnValPrrhIsgLysArgValPheLys | 687 |
| Db | 1369 | ATGTACTTCCAACTGCTGGGCGGCTGATTAAGACACAACTCAACCCCAATGAAGCGCTTCCAA | 2028 |
| QY | 688 | AlaSerArgSerAsnAsnAsnPheArgPheMetGlyLeuLeuLeuLeuValLeuPheLeuSerLeu | 707 |
| Db | 2029 | GGCTCCCGAATCCAAACACTTCTCACTGGGCGCTCTGCTGCTGGTCTCTTCTCAGGCTTC | 2088 |
| QY | 708 | LeuPrrpValAlaLysTrrhLeuMetSerLeuPrrpPrrpSerPheAspCysGlyPrrpPheSer | 727 |
| Db | 2089 | CTGGCGGCTGGCTCAACCAATCATGTCCCTCCACCGCTCTTGACTGGCGGCGCTTCACT | 2148 |
| QY | 728 | GlyLysAsnArgMetCysArgPrrpValLeuGlnGlnLysTrpGluAsnAsnAsnAsnAsnAsn | 747 |
| Db | 2149 | GGGAAAAACAAAGTACCACTCTCTCCAAAGACAACTGAAAAAGATTTCCCAACCTTTC | 2208 |
| QY | 748 | LeuGlyLysTrpPheAlaPheLeuValAsnPrrpGlyLeuLeuLeuLeuLeuLeuLeu | 767 |
| Db | 2209 | CTGGGCAAGATCTTGGCTTCTCTGGCAATCCAGGCGCTGATCATCCAGCATCTCTGCTG | 2268 |
| QY | 768 | MetPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu | 787 |
| Db | 2269 | ATGTTCTTGGCCATTTTACTACTGAACTCACTGATCTTCCAAAGGCTTCTCCGAACTAAAGCC | 2328 |
| QY | 788 | GlnLeuArgLysLysLysLeuGlnValLeuArgGlyValGluLysSerHisLysSerValLys | 807 |
| Db | 2329 | CAGCTGAGGAAGAAATCCAACTGCTCTCGTGAAGTTGAGAAAGATCACAAACTCTGTA | 2388 |
| QY | 808 | GlyLysAlaThrAlaArgAspSerGluAsnTrpLysSerSerSerLysAsnAlaThr | 827 |
| Db | 2389 | GGCAAGCCACAGCCAGATTTACAGAGACACACTAAAGGAGCTCCAAAAATGCCACC | 2448 |
| QY | 828 | GlnLeuGlnLeuThrLysGluGluTrpTrpPrrpPrrpSerAlaSerGlnSerGlnAlaMet | 847 |
| Db | 2449 | CAGCTCCCACTCAACAAAGAAAGACCACTCTCTCTCTGGCCACCAAAAGCCAGGCAATG | 2508 |
| QY | 848 | AspLysLysAlaGlnGlyProGlyTrpHisSerAsnSerAlaSerArgTrpThrLeuPrrpAla | 867 |
| Db | 2509 | GACAAAGAGGCGCAGGGCCCTGGGACCTCCAAATTCGCAAGAGACCACTGCTGCTGC | 2568 |
| QY | 868 | SerGlyHisLeuPrrpLysSerArgPrrpPrrpGlyLysGlyPrrpAspSerGlyHisAlaPrrp | 887 |
| Db | 2569 | TCGGACACCTTCTCTAATCTGGGCGCCCTGGAAATCGAGACAGATTCCTGGCCAGCGCCCA | 2628 |
| QY | 888 | SerGlnHisLysPrrpTrpArgSerAlaSerGlyLysSerLysLysLysLysLysLysLys | 906 |
| Db | 2629 | TCTCAGACTCATCGTGGAGGTCAAGCTCTGGAAAGAGGTCTCAAGACCTTCCCAAC | 2685 |

APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyun
APPLICANT: Drennan, Radcliffe T.
TITLE OF INVENTION: No. US20030219743A1ol Nucleic Acids and
FILE REFERENCE: Polypeptides
CURRENT APPLICATION NUMBER: US/10/115,831
CURRENT FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: 09/667,298
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/577,408
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 178
SOFTWARE: pc FL_genes Version 2.0
SEQ ID NO 134
LENGTH: 4895
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(4785)
US-10-115-831-134

Alignment Scores:
Prod. No.: 0 Length: 4895
Score: 583.00 Matches: 583
Percent Similarity: 100.00% Conserved: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 64.35% Indels: 0
DB: 6 Gaps: 0

US-10-792-307-4 (1-906) x US-10-115-831-134 (1-4895)

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DB 1096 GGCTATATCAAGTACTGCACTCTCTATGGCTACACAAACAGAGAGCCATCGGG 1155
QY 332 TRPLEAUGTYRARGLEUPROMECALATYRPHMEVALGILVALSERVALPHOGLYTYR 351
DB 1156 TGGCTGAGGTACCGGCTGCTATGGCTACTTATGGTGGGGGTCAACGCTTCGGCTAC 1215
QY 352 SERLEUILEILEVALILEARGSERMECALASERANTHCHINGLYSERTHGLUGLY 371
DB 1216 AGCTGATTATGTCAATTCATCGATGGCAGCAATACCCAAAGAGCAAGCGGAGGG 1275
QY 372 GLUSERASPANPHETHPHESERPHELYSHEPHETHPHETHPHAPTYRLEUILEGLY 391
DB 1276 GAGGTGACAACTTCACATTCAGCTTCAGAGATGTTACACAGCTGGAGCTACTGATCGGG 1335
QY 392 AANSEGLUTHRALASPANLYTYRALASERILLETHRTHSERPHELYSGLUSERILE 411
DB 1336 AATTCAGACACGCTGATACAAATATGATCCATCACCAACGCTTCAAGGATCAATA 1395
QY 412 VALASPGIUGIUGISERANLYSGIUGIUGANILEHISLEUTHRARGPHLEUKYVAL 431
DB 1396 GTGGATGAACAGAGGTAAACAAAGAGAAATATCCATCTGACAGATTCTTCGTCTC 1455

QY 432 LEUVALASPHEUILEILECYSCYSEUQGLYSERGLYTYRLEUILETYRPHVAL 451
DB 1456 CTGGCAACTTCTCATCATCATCTGCTGTTTGTGGAGAGGGATACCTCATTTACTTGTGTC 1515
QY 452 VALLYSARGSERCHINGINPHESERYSMEGCHNANVALSERTPYRGLUGARGANGLY 471
DB 1516 GTTAAAGGATCTCAGCAATTTCTCCAAATGCAATGTCAGCTGGATGTAAGAGAAATGAG 1575
QY 472 VALGIUILEVALMESERLEUQGLYMEPHCYAPROPHLEUPHETHTHLEALE 491
DB 1576 GTAAAGATCGTATGTCCTGCTGCTGGAATGTTTGTCCCTCTGTTTAAACCATCGCT 1635
QY 492 ALALEUGIUGANTYRHSIPROARGTHRGILYUPLYSTPRGILNLEUGLYARGI1EPHEALA 511
DB 1636 GCCCTGAGAAATTACCAACCCACGCTGAGCTGAAGTGGCAGCTGGGACCATCTTTGCA 1695
QY 512 LEUPHEUQGLYANLEUITYRTHRPHLEUQGLYALEUWECAPAPYVALHISLEUPLY 531
DB 1696 CTTTCTGGGGAACCTCTACACATTTCTCTGGCCCTGATGATGTCACACTCAAG 1755
QY 532 LEUVALASPNGIUGIUTHRILEYSPANILETHRHSIPRTHRLEUPHESANTYRTPAN 551
DB 1756 CTTGCTAATGAGAGACATMAAGAACATCACTCACTGAGACTGTTTAACTATTACAC 1815
QY 552 SERSEGLYTRPANSGLUSERVALPROARGPROLEUHSIPROALASPVALPROARG 571
DB 1816 TTTCTGTTGGAAGAGAGTGTCCCGGACACCCCTGCACCTCGACAGATGTGCCCGG 1875
QY 572 GLYSERCYSTPRGILUTHRALVALGILYILEGLUPHMECALAGLEUTHRALSERAPHEC 591
DB 1876 GGTCTTGTGGAGACAGCTGTGGGCAATTGAATTCATGAGGCTGACGGTGTGACATG 1935
QY 592 LEUVALTHRTYRILETHRILELEUQGLYASPPHELEUARGALACYSPHEVALACGPH 611
DB 1936 CTGGAAACGATACATCAATCATCTGCTGGGGGACTTCTACAGGCTGTTTGTGCGGTTTC 1995
QY 612 MECHANITYRCYSTPRCYSYTRPASPLEUGIUGILEYPHNEPROSEYTRALGILUPHEAP 631
DB 1996 ATGAACCTACGCTGCTGCTGGAGCTTGGAGGCTGGATTTCTTCATATGCTGAGATTGAT 2055
QY 632 ILESERGLYASNVALLEUGIYLEUILEPHASNGINGLYMETILETRPHEGLYSERPH 651
DB 2056 ATTAGTGAAGATGTGCTGGGTTGATCTTCAACCAAGAGATGATCGATGGGCTCTTC 2115
QY 652 TYRALAPROGLYLEUVALGILYILEASNVALLEUARGLEUUTHRSEMECTYRPHENGLIN 671
DB 2116 TATGCTCAAGGCTGCTGGGCAATTAATGTGCTGCGCTCGTGAACCTCACTACTTCAG 2175
QY 672 CYSYTRPALVALMESESERSEANVALPROHISGLUGARGVALPHELYALASERARGSEAR 691
DB 2176 TCTGTGGGCGGTGATGAGAGCAACGTACCCCAAGAACCGGTGTTCAAAGCCTCCCAATCC 2235
QY 692 AANAPHEUTHERGILYLEUWECLEUWELVALLEUPHEUQGLYSEUQGLYVALALA 711
DB 2236 AACCACTTCAACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2295

| | | |
|--|--------------------|--|
| ? | SOFTWARE: | Custom |
| ? | SEQ ID NO | 28100 |
| ? | LENGTH: | 5027 |
| ? | TYPE: | DNA |
| ? | ORGANISM: | Homo sapiens |
| ? | FEATURE: | |
| ? | NAME/KEY: | SIMILAR |
| ? | LOCATION: | (1906)..(2340) |
| ? | OTHER INFORMATION: | 100% homologous to Homo sapiens dJ68663.3 (novel) |
| ? | OTHER INFORMATION: | gene, accession number AL049712, Smith-Waterman Score=778 |
| US-10-450-763-28100 | | |
| Alignment Scores: | | |
| Pred. No.: | 0 | Length: 5027 |
| Score: | 583.00 | Matches: 583 |
| Percent Similarity: | 100.00% | Conservative: 0 |
| Best Local Similarity: | 100.00% | Mismatches: 0 |
| Query Match: | 64.35% | Indels: 0 |
| DB: | 9 | Gaps: 0 |
| US-10-792-307-4 (1-906) x US-10-450-763-28100 (1-5027) | | |
| QY | 312 | GLYTYRLLQLYTYRSERALEUPHETRYGLYTRYASMANGLNRGTHLLGLY 331 |
| DB | 1096 | GGCATATCAAGTACTCTGCATCTCTATGGCTACTACACACCAAGGAGCATCTGGG 1155 |
| QY | 332 | TFPLEUARYTYAGLEUPHOKHEVALTYRPHHEVALGLVALSERALPHAGLYTYR 351 |
| DB | 1156 | TGGCTAGGTACCGGCTGGCTTGGCTTACTTATGGTGGGGGTCAAGCTGTGGCTAC 1215 |
| QY | 352 | SERLEULLLEVALLEALRGSERMEALSERANTHRGLNGLSERTHLYGLUGLY 371 |
| DB | 1216 | ACCGTATTTATGTCATTCGATCACTGCCACCAATACCAAGGAGACAGCGAAGGG 1275 |
| QY | 372 | GLUSERAPAPHPHETHRPHESEPHYSMETHESERTTPAPRYTLEULLGLY 391 |
| DB | 1276 | GAGGTGACCACTTCACTTCACTGCTTCAAGATGTTCCACAGCTGGAGCTACCTATCGG 1335 |
| QY | 392 | AANSEFGIUTHALAEAPANLYATYALASERILLETHRSERPHELYSGLUSERILE 411 |
| DB | 1336 | AATTCAGACAGACGCTGATAACAAATATGCATCTCAACCAACGACGTTACAGGAATCA 1395 |
| QY | 412 | VALAPGLUGLNGLSERANLYSGIUGLUNANILLELSEUETHRARGHELEUPAL 431 |
| DB | 1396 | GTGATGACCAAGAGATTAACAAAGAAATATCCATCTGACAGATTCTTCGTGTC 1455 |
| QY | 432 | LEMLAPAPHPHEULLLEQVSCYCLEUQVGLYSERGLYTYRLEULLTQRYPHOVAL 451 |
| DB | 1456 | CTGGCGAACCTTCTCACTCATCTCGCTGTTGTGTGGAAGGGGTACCTCACTTACTTGTG 1515 |
| QY | 452 | VALLYSARESERGINGINPHESELYRMEQGINANVALSERTPRYCOLUARGANGLU 471 |
| DB | 1516 | GTTAAGGATCTCAGCAATTCCTCCAAATGCGAAGATGTCAGCTGTATGAAAGGAATGAG 1575 |
| QY | 472 | VALGLULLEVALHETSERLEULEUGLYHETHECYAPROPLEUAPHEGLUTHILLEAL 491 |
| DB | 1576 | GTAAAGATGATGATGCTCGCTGTGAATGTTTGTCCCGCTGTTTAAACCATCGCT 1635 |

QY 492 ALeIeuGubAnTyRhiSProArGThRgIeUySTrPGLnLeuGIArGrlIePhAla 511
 Db 1636 GCGCTGAGAAATTACAGCCAGCGACTGAAAGTGGAGCTGGAGCACTCTTGA 1695
 QY 512 LeuPheLeuGlyAnLeuTyRThRPhelLeuAlaLeuKerAspAspValHisLeuLys 531
 Db 1696 CTCTCTCGGGGAACCTCTACACATTTCTTGGCCCTGATGATGAGCGTCCACCTCAAG 1755
 QY 532 LeuAlaAnGluGluThRLeuValAnIleThRhiSTrThRLeuPheAnTyRAsp 551
 Db 1756 CTGGCTAAATGAGAGCAATTAAGACATCACTGACCTCTGTTAACTATTACAC 1815
 QY 552 SerSerGlyTrpAnGluSerValProArGProLeuHisProAlaAspValProArG 571
 Db 1816 TCTTCTGGTTGAAACAGAGTGTCCCGCAGACCCCTGCACCGTGAATGTGCCCGG 1875
 QY 572 GlySerCysTrpGluThRAlaValGlyIleGluPheKerAArgLeuThRValSerAspMet 591
 Db 1876 GGTTCTGCTGGGAGACAGCTGGGCATTGAATTCATGAGCGTGAAGGTGTGACATG 1935
 QY 592 LeuValThRTyrIleThRLeuLeuGlyAspPheLeuArgAlaCysPheValArgPhe 611
 Db 1936 CTGGTAACGTACATCACTCACTGCTGGGGGACTTCTTACGGGCTGTGTTGTGGGTTG 1995
 QY 612 MetAnTyRcysTrpCysTrpAspLeuGluAlaGlyPheProSerTyAlaGluPheAsp 631
 Db 1996 ATGAACCTACTGCTGGTGGGACTTGGAGCTGGATTCCTCTCATATGCTGAGTTGAT 2055
 QY 632 IleSerGlyAnValLeuGlyLeuIlePheAnGlnGlyMetIleTrpMetCysSerPhe 651
 Db 2056 ATTAGTGAATAATGCTGGGTTGATCTTCAACCAAGAAATGATCTGATGGGCTCCTTC 2115
 QY 652 TyrAlaProGlyLeuValGlyIleAnValLeuArgLeuThRSerMetTyRPhGln 671
 Db 2116 TATGCTCCAGGCTGGTGGGCAATTATGCTGGCCCTGCTGACCTCATGTACTTCAG 2175
 QY 672 CysTrpAlaValMetSerSerAnValProHisGluArgValPheLysAlaSerArgSer 691
 Db 2176 TGCTGGCGGCTGATGAGCAGCACTGACCCCATGAACGCTGTTCAAAAGCCTCCCGATCC 2235
 QY 692 AsnAnPheTyRMetCysLeuLeuLeuValIleuPheLeuSerLeuLeuProValAla 711
 Db 2236 AACAACTTCTACATGGGCTCTGCTGCTGGTGTCTCTCTCAGGCTCTGCGGGTGGCC 2295
 QY 712 TyrThrIleMetSerLeuProSerPheAspCysGlyProPheSerGlyLysAnArg 731
 Db 2296 TACACCATCATGTCCCTCCACCTCTTGACTGGGGGCGTTCACTGGAAAAACAGA 2355
 QY 732 MetTyRAspValLeuGlnGluThRleGluAnAspPheProThRPhelGluGlyLysIle 751
 Db 2356 ATGTACGATGTCTCCAAAGAACCATTTGAAAACAATTTCCCAACCTTCTGGGCAAGATG 2415
 QY 752 PheAlaPheLeuAlaAnProGlyLeuIleIleProAlaIleLeuLeuPhePheLeuAla 771
 Db 2416 TTTCCTTTCTCCCAATCCAGGCTGATCATCCAGACCATCCTGCTGATGTTCTTGGCC 2475

QY 772 IleTyTyRLeuAnSerValSerLysSerLeuSerArgAlaAnAlaGlnLeuArgLys 791
 Db 2476 ATTACTACCTCACTGACTGATTTCCAAAAAGCTTTCCGAGCTAATGCCACGCTGAGGAG 2535
 QY 792 LysIleGlnValLeuArgGluValGluLysSerHisLysSerValLysGlyLysAlaLeu 811
 Db 2536 AAAATCCAACTGCTCCGTAAGATTGAGAGAGTCAAAATCTGTAAAGCAAAAGCCACA 2595
 QY 812 AlaArgAspSerGluAspThRProLysSerSerSerLysAnAlaThRglnLeuGlnLeu 831
 Db 2596 GCGAGATTCAGAGAGACACCTTAAGAGCTCCAAATAATGCCACCCAGCTCAACTC 2655
 QY 832 ThrLysGluGluThRThRProProSerAlaSerGlnSerGlnAlaValAspLysVala 851
 Db 2656 ACCAAGAGAGACCACTCCCTCTGCCAGCAAAAGCAGGCAATGGAGCAAGAGCGG 2715
 QY 852 GlnGlyProGlyThRSerAnSerAlaSerArgThRThRLeuProAlaSerGlyHisLeu 871
 Db 2716 CAGGACCTGGAGCTCCAAATCTGCAAGCAGACCACTGCTGCTGAGACCTT 2775
 QY 872 ProIleSerArgProProGlyIleGlyProAspSerGlyHisAlaProSerGlnThRHis 891
 Db 2776 CCTATATCTGGGCCCCCGAATCGGACCAAGATTCTGGGCAAGGCCCATCTCAGACTCAT 2835
 QY 892 ProTrpArg 894
 Db 2836 CCGTGGAGA 2844

RESULT 5
 US-10-108-260A-342
 ; Sequence 342, Application US/10108260A
 ; Publication No. US2004005560A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: No. US2004005560A1el full length cDNA
 ; FILE REFERENCE: HI-A0106
 ; CURRENT FILING DATE: 2002-03-27
 ; NUMBER OF SEQ ID NOS: 5458
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 342
 ; LENGTH: 2560
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-108-260A-342

Alignment Scores:
 Pred. No.: 1,62e-188 Length: 2560
 Score: 198.00 Matches: 198
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 21.85% Indels: 0
 DB: 6 Gaps: 0

US-10-792-307-4 (1-906) x US-10-108-260A-342 (1-2560)
 QY 427 ArgPheLeuArgValLeuAlaAnPheLeuIleIleCysCysLeuCysGlySerGlyTyR 446

DB 2 AGATTCTTCGTGCTGCTGCGCACTTTCATCATCTGCTGTTGTGTGGAAGTGGGTAC 61
QY 447 Leu11eTyPheValValLysArgSerGlnGlnPheSerLysMetGlnAanValSerTrp 466
DB 62 CTCATTACTTGTGTGCTTAAGGATCTCAAGCAATTCACCAAAATGCAAAATGTCAGCTGG 121
QY 467 TyrGluArgAsnGluValGlu11eValMetSerLeuLeuGlyMetPheCysProProLeu 486
DB 122 TATGAAGGAATGAGGTAGAGATGCTGATGCTCCCTGCTTGGAATGTTTGTCCCTCTG 181
QY 487 PheGluTrn11eAla1AlaLeuGluAanTyRhiSProArgThGlyLeuLysTrpGlnLeu 506
DB 182 TTGAAACCATGCTGCTGCTGGAAGATTACACCCACGCACTGGAGTGGCAAGCTG 241
QY 507 GlyArg11ePheValLeuPheValLeuGlyAanLeuTyRhiPheLeuValAlaLeuMetCys 526
DB 242 GAGCGCATCTTGCACTCTTCTGCGGAACCTCTACACATTTCTCTTGCGCCCTGATGGAT 301
QY 527 AspValH1sLeuLysLeuAlaAsnGluGluTrn11eLysAan11eThrH1sTrpThrLeu 546
DB 302 GATGTCCAGCTCAAGCTTGCTATGAAAGAGCAATTAAGACATCACTCACTGAGCTCTG 361
QY 547 PheAanTyRhiArgSerSerClyTrpAanGluSerValProArgProProLeuH1sPro 566
DB 362 TTTAACATTACAACTCTTCTGTTGGAACGAGGTGCCCCGACACCCCTGACCTG 421
QY 567 AlaAspValProArgGlySerCysTrpGluTrnAlaValGly11eGluPheMetCysLeu 586
DB 422 GCGATGTGCCCCGGGTTCTTGTGCTGGAGACAGCTGTGGGATTTGAATTCAGAGCTG 481
QY 587 ThrValSerAspMetLeuValThrTyRhi11eLeuLeuGlyAspPheLeuArgAla 606
DB 482 ACCGTGTCCGACATGCTGTGATACGTACATCACCATCTGCTGGGGGACTTCTTAAGGGCT 541
QY 607 CysPheValLeuPheMetCysTyRhiCysTrpCysTrpAspLeuGluAlaGlyPhe 624
DB 542 TGTTTGTGCGGTTCACTGACTGCTGTGGGACTTGAAGGCTGGAATTT 595

RESULT 6
US-10-487-887-7
; Sequence 7, Application US/10487887
; Publication No. US20040249139A1
; GENERAL INFORMATION:
; APPLICANT: Griffith, Andrew J
; APPLICANT: Kurimay, Kiyoto
; APPLICANT: Wilcox, Edward
; APPLICANT: Friedman, Thomas
; TITLE OF INVENTION: TRANSDUCTIN-1 AND TRANSDUCTIN-2 AND APPLICATIONS TO
HEREDITARY
; TITLE OF INVENTION: DEAFNESS
; FILE REFERENCE: 226544
; CURRENT APPLICATION NUMBER: US/10/487,887
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/US02/29614
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/323,275

; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 3216
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-487-887-7
Alignment Scores:
Pred. No.: 1,42e-88 Length: 3216
Score: 99.00 Matches: 140
Percent Similarity: 98.59% Conservative: 0
Best Local Similarity: 98.59% Mismatches: 1
Query Match: 10.93% Indels: 2
DB: Gaps: 0
US-10-792-307-4 (1-906) * US-10-487-887-7 (1-3216)
QY 213 MetAlaLeuLysTrpValLysPheLysArgAspPheAspAanPheLysThrGlnCys11e 232
DB 904 ATGGCTAAGAAATGGGTCAAGTTTAAAGGGGACTTGATTAATTTCAAGACTCAATGATAT 963
QY 233 ProTrpGluMetCys11eLysAsp11eGluSerH1sPheGlySerSerValAlaSerTyR 252
DB 964 CCTGGGAATGAAGATCAAGACATTGAAAGTCACTTGCTGCTGCTGCTGCTGCTTAC 1023
QY 253 Phe11ePheLeuArgTrpPheCtyrGlyValAanLeuVal11ePheGlyLeu11ePheGly 272
DB 1024 TTCACTCTTTCGCAATGGAATGATGGAATTAACCTTGCTCTTTTGGCTAAATTTGGT 1083
QY 273 LeuVal11e11eProGluValLeuMetGlyMetProTyRolySer11eProArgLysThr 292
DB 1084 CTAGTCATCATCCACGAGGTGCTGATGGGCATGCCCTATGGAAGTATACCCAGAAAGACG 1143
QY 293 ValProArgAlaGluGluGlyLys-AlaMetAspPheSerValLeuTrpAspPheGlu 312
DB 1144 GTGCTGAGACTGAGGAAAGCG-AGCCATGAGACTTCTGTCTTGTGGATTTTGAAGG 1202
QY 312 YTyR11eLysTyRSerAlaLeuPheTyR11eTyRAsnAsnGlnArgThr11eGlyTr 332
DB 1203 CTACATCAAAATATCTGCTCTCTCTATGCTACTACAAACAACAGGACCATGATGATG 1262
QY 332 PLeuArgTyRArgLeuProMetAlaTyRPhMetValGlyValSerValPheGlyTyRSe 352
DB 1263 GCTGAGGTACAGGCTGCCCATGGCTTACTTATGTGTGGGGGTCAAGCTGTTGGCTACAG 1322
QY 352 rLeu 353
DB 1323 CTTG 1326

RESULT 7
US-10-792-307-7
; Sequence 7, Application US/10792307
; Publication No. US20050196759A1
; GENERAL INFORMATION:
; APPLICANT: Griffith, Andrew J.

; APPLICANT: Kurima, Kiyoto
; APPLICANT: Wilcox, Edward
; APPLICANT: Friedman, Thomas
; TITLE OF INVENTION: TRANSDUCTIN-1 AND TRANSDUCTIN-2 AND APPLICATIONS TO
HEREDITARY
; TITLE OF INVENTION: DEAFNESS
; FILE REFERENCE: 227340
; CURRENT APPLICATION NUMBER: US/10/792,307
; CURRENT FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 3216
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-792-307-7

Alignment Scores:
Pred. No.: 1,42e-88 Length: 3216
Score: 99.00 Matches: 140
Percent Similarity: 98.59% Conservative: 0
Best Local Similarity: 98.59% Mismatches: 1
Query Match: 10.93% Indels: 2
DB: 9 Gaps: 0

US-10-792-307-4 (1-906) x US-10-792-307-7 (1-3216)

QY 213 MetAlaIySlySTrpValIySPhelYsArGAspPheAspAnPheIySThrGInCyAlE 232
|||
Db 904 ATGGCTAAGAAATGGGTCAAGTTTAAAGAGGACTTGTATTAATTCCAAGACTCAATGTAATT 963
|||
QY 233 ProTrpGluMetIySIlElySAspIleGluSerHisPheGlySerSerValAlaSerTyr 252
|||
Db 964 CCCTGGGAAATGAAGATCAAGACATTGAAGTCACTCGGTTCTCTGTGGCATCTTAC 1023
|||
QY 253 PheIlePheLeuAgtTrpMetTyrGlyValAsnLeuValLeuPheGlyLeuIlePheGly 272
|||
Db 1024 TTCATCTTCTCCGATGGATGTATGAGATTAACTGTCTTTGGCTTAATATTGGT 1083
|||
QY 273 LeuValIleIleProGluValLeuMetGlyMetProTyrGlySerIleProArgIySThr 292
|||
Db 1084 CTAGTCATCATCCACAGAGGTGCTGATGGGCATGCCCATGGAAGTATACCGAAGAAAGCG 1143
|||
QY 293 ValProArgAlaGluGluGluIyS-AlaMetAspPheSerValLeuTrpAspPheGluGlu 312
|||
Db 1144 GTGCCTCGAGCTGAGGAAAGCG-AGCCATGGACTTCTGTGCTTTGGGATTTGAGGG 1202
|||
QY 312 yTyrIleIySerAlaLeuPheTyrGlyTyrTyrAsnAsnGlnArgThrIleGlyTyr 332
|||
Db 1203 CTACATCAAAATATTGCTGCTCTTCTATGGCTACTACAAACAAACGCGACCATTTGGATG 1262
|||
QY 332 pLeuArgTyrArgLeuProMetAlaTyrPheMetValGlyValSerValPheGlyTyrSe 352
|||
Db 1263 GCTGAGGTACAGGCTGCCCATGGCTTACTTATGTGTGGGGGTCAAGCGTGTGGCTACAG 1322
|||
QY 352 rLeu 353
|||

Db 1323 CTGTG 1326

Search completed: December 5, 2005, 05:00:34
Job time : 1494 secs

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 23:39:38 ; Search time 588 Seconds
(without alignments)
479.533 million cell updates/sec

Title: US-10-792-307-4

Perfect score: 906
Sequence: 1 MSHQVKGKKEARGVGKRV.....PSQTHPMVSASGSAQRPPI 906

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3289935 seqs, 155610033 residues

Word size: 70

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10792307/runat_23112005_080817_19853/app_query.fasta_1
.1095
-DB=Published_Applications_NA_New:*
-MINMATCH=0.1 -LOOPTL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=quality -THR_MIN=70
-ALIGN=15 -MODE=LOCAL -OUTFMT=pic -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10792307.qcgn 1.1 184 @runat_23112005_080817_19853
-NCPUP=6 -ICPU=3 -NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

Published_Applications_NA_New:*
1: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|---------------|-------|----------------|--------|----|-------------|
|---------------|-------|----------------|--------|----|-------------|

No matches found

Search completed: December 5, 2005, 05:10:03
Job time : 589 secs

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

OM protein - nucleic search, using frame_plus_p2n model

SUMMARIES

Run on: December 4, 2005, 22:52:13 ; Search time 7245 Seconds
(without alignments)
5650.807 Million cell updates/sec

Title: US-10-792-307-4
Perfect score: 906
Sequence: 1 MSHQVKGLEKAEKRGVKGKV.....PSQTHPWSASGKSAGRPPI 906

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Word size: 70

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame_plus_p2n.model -DEV=x1p
-O=/cgr2_1/USPRO_spool_p/US10792307/runat_23112005_080815_19776/app_query.fasta_1.1095
-DB=EST -QFMT=fastap -SUFFIX=p2noligo.rcst -MINMATCH=0.1 -LOOFCU=0 -LOOFEEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=quality -THR_MIN=70 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10792307 @CGEN 1.1 8010 @runat 23112005 080815 19776 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

1: gb_gst1: +
2: gb_gst2: +
3: gb_gst3: +
4: gb_hic: +
5: gb_gst4: +
6: gb_gst5: +
7: gb_gst6: +
8: gb_gst7: +
9: gb_gst8: +
10: gb_gst9: +
11: gb_gst10: +

| Result No. | Query | | | | Description |
|------------|-------|-------|--------|----|--------------------|
| | Score | Match | Length | ID | |
| 1 | 102 | 11.3 | 1827 | 10 | AY406224 Homo sapi |
| 2 | 89 | 9.8 | 1827 | 10 | AY406226 Mus muscu |
| 3 | 80 | 8.8 | 247 | 6 | CD635963 56089332H |
| 4 | 80 | 8.8 | 247 | 6 | CD635964 56089332J |

ALIGNMENTS

RESULT 1
LOCUS AY406224
DEFINITION Homo sapiens TM22 gene, VIRTUAL TRANSCRIPT, partial sequence.
ACCESSION AY406224
VERSION AY406224.1 GI:39762198
KEYWORDS GSS.
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 1827)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kojariwal, A., Todd, M.A., Tenenbaum, D.M., Clevello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J., Adams, M.D. and Cargill, M.
TITLE Interfering nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1827)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kojariwal, A., Todd, M.A., Tenenbaum, D.M., Clevello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J., Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
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REFERENCE 1 (bases 1 to 247)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
PUBMED 15203218
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES
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RESULT 4
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LOCUS 56089332J1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION

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Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 247)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
PUBMED 15203218
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
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Score: 80.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.83% Indels: 0
DB: Gaps: 0
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Job time : 7248 secs

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 17:37:51 ; Search time 10018 Seconds

(without alignments)
5140.763 Million cell updates/sec

Title: US-10-792-307-4

Perfect score: 4744
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: gb_in:1
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15: gb_pl:1

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 3139.5 | 66.2 | 3066 5 AY561309 | AY561309 Gallus ga |
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| 8 | 2300 | 48.5 | 2895 9 AF417579 | AF417579 Mus muscu |
| 9 | 1692.5 | 35.7 | 6222 9 AY263157 | AY263157 Mus muscu |
| 10 | 1678.5 | 35.4 | 4746 8 AY263163 | AY263163 Homo sapi |
| 11 | 1675 | 33.3 | 3495 5 AY361310 | AY361310 Gallus ga |
| 12 | 1657.5 | 34.9 | 2442 8 AY236490 | AY236490 Homo sapi |
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| 17 | 1374.5 | 29.0 | 884 6 CQ728483 | CQ728483 Sequence |
| 18 | 1167 | 24.6 | 2276 6 CQ734586 | CQ734586 Sequence |
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| 21 | 1120.5 | 23.6 | 5929 6 CQ578280 | CQ578280 Sequence |
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| 24 | 928.5 | 19.6 | 1528 8 AK098607 | AK098607 Homo sapi |
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| 35 | 638.5 | 13.5 | 3504 8 AY264698 | AY264698 Homo sapi |
| 36 | 633.5 | 13.4 | 2384 8 BC047719 | BC047719 Homo sapi |
| 37 | 624 | 13.2 | 2330 9 AY236499 | AY236499 Mus muscu |
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| 39 | 617.5 | 13.0 | 2465 8 AB168722 | AB168722 Macaca fa |
| 40 | 617.5 | 13.0 | 3013 5 AY561312 | AY561312 Gallus ga |
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43 602 12.7 2511 5 AY263173 Takifugu
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ALIGNMENTS

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LOCUS Homo sapiens transmembrane channel-like protein 2 (TM2) mRNA,
DEFINITION complete cds.
ACCESSION AF417580
VERSION AF417580.2 GI:28642834
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Kurima, K., Peters, L.M., Yang, Y., Riazuddin, S., Ahmed, Z.M., Naz, S.,
Arnold, D., Drury, S., No, J., Makishima, T., Ghosh, M., Menon, P.S.N.,
Deshmukh, D., Oddoux, C., Osterer, H., Khan, S., Riazuddin, S.,
Delinger, P.L., Hampton, L.L., Sullivan, S.L., Battey, J.F.,
Keats, B.J.B., Wilson, E.R., Friedman, T.B. and Griffith, A.J.
TITLE Dominant and recessive deafness caused by mutations of a novel
gene, TM2, required for cochlear hair-cell function
JOURNAL Nat. Genet. 30 (3), 277-284 (2002)
PUBMED 11850618
REFERENCE
AUTHORS Kurima, K., Griffith, A.J. and Friedman, T.B.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-2001) NIDCD, NIH, 5 Research Court, #2A02,
Rockville, MD 20850, USA
REFERENCE
AUTHORS Kurima, K., Griffith, A.J. and Friedman, T.B.
TITLE Direct Submission
JOURNAL Submitted (03-MAR-2003) NIDCD, NIH, 5 Research Court, #2A02,
Rockville, MD 20850, USA
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COMMENT Sequence update by submitter
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ORIGIN

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US-10-792-107-4 (1-906) x AF417580 (1-3169)

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RESULT 2
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DEFINITION Mus musculus transmembrane channel-like protein 2 (Tmc2) mRNA,
complete cds.
ACCESSION AF417581
VERSION AF417581.1 GI:19223984
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 3216)
AUTHORS Kurima,K., Peters,L.M., Yang,Y., Riazuddin,S., Ahmed,Z.M., Naz,S.,

Arnaud,D., Drury,S., Mo,J., Makishima,T., Ghosh,M., Menon,P.S.N.,
Deshmukh,D., Oddoux,C., Oester,H., Khan,S., Riazuddin,S.,
DeLinger,P.L., Hampton,L., Sullivan,S.L., Battey,J.F.,
Keates,B.J.B., Wilcox,E.R., Friedman,T.B. and Griffith,A.J.
Dominant and recessive deafness caused by mutations of a novel
gene, TMC2, required for cochlear hair-cell function
Nat. Genet. 30 (3), 277-284 (2002)
JOURNAL
PUBMED 11850618
REFERENCE 2 (bases 1 to 3216)
AUTHORS Kurima,K., Griffith,A.J. and Friedman,T.B.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-2001) NIDCD, NIH, 5 Research Court, #2A02,
Rockville, MD 20850, USA
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QY 121 ProArgLysGluGluLysSerLysArgGlnLysArgProArgSerSerSerLeuAlaSer 140
Db 631 CTGAGGAAG--GAGGACGGCAAGCAGCTGAGAAACCCAGGTCCTCTTGGGCTCC 687
QY 141 SerAlaSerGlyGlyLysSerLeuSerGluGluGluLeuAlaGlnLeuGluGluVal 160
Db 688 AGTGTCTACTAGAACTCCCTGTCTGAGAGAGAGCTGGCTCAGATCCTGAGACAGTA 747
QY 161 GluGluLysLysLysLeuAlaAlaThrPheCArgSerLysProThrPheCAlaLysLys 180
Db 748 GAAGAAAAAGAAAGCTCATCACTGAGGAAACAAACCTGGCCCATGGCAAGAGAG 807
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Db 808 CTGAGGAACTCAAGGAAAGCCCAAGCCTTTGTGAGAGATATGAAAGAGCCTTGGGAGAA 867
QY 201 GlyLysGlyLysGlnLeuTyrAlaTyrLysPheCLeuPheCAlaLysLysTyrValLysPhe 220
Db 868 GGCAGGGCAAAACACTCTACGCCTACAGATGATGATGGCTAAGAAATGGGTCAAGTTT 927
QY 221 LysArgAspPheAspAsnPheLysThrGlnCysIleProThrGluPheClysIleLysAsp 240
Db 928 AAGAGGCACTTGTATATTCAAGCTCAATGTATCCCTGGGAAATGAAGATCAAGAAC 987
QY 241 IleGluSerHisPheGlySerSerValAlaSerTyrPheIlePheLeuArgThrPheC Tyr 260
Db 988 ATTGAAAGTCACTGGGTTCTTCTGTGGCACTTAATCTCACTTTTCTCCGATGGATGTAT 1047
QY 261 GlyValAsnLeuValLeuPheGlyLeuIlePheGlyLeuValIleIleProGluValLeu 280
Db 1048 GAGTTAACTTGTCTTTGGCTTAATTTGGTCTAGTCATCATCCCAAGGTCGTG 1107
QY 281 MetGlyMetProTyrGlySerIleProArgLysThrValProArgAlaGluGluGluLys 300
Db 1108 ATGGCATGCCCTATGGAAGTATACCCAGAAAGAGGTCCTCGAGCTGAGGAGAGACGCA 1167

QY 301 AlaMetAspPheSerValLeuThrAspPheGluGlyTyrIleLysTyrSerAlaLeuPhe 320
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QY 321 TyrGlyTyrTyrAsnAsnGlnArgThrIleGlyTyrPheLeuArgTyrArgLeuProMetAla 340
Db 1228 TATGGTACTACAAACAAACAGCGGACCATTTGATGGCTGAGGTATCAGGCTCCCATGGCT 1287
QY 341 TyrPheMetValGlyValSerValPheGlyTyrSerLeuIleIleValIleArgSerMet 360
Db 1288 TACTTATGGTGGGGGTACCGGTGTTTGGCTACAGCTTGAATCTCATTAAGTGCATG 1347
QY 361 AlaSerAsnThrGlnGlySerThrGlyGluGlyLysSerAspAsnPheThrPheSerPhe 380
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QY 381 LysPhePheThrSerTyrAspTyrLeuIleGlyAsnSerGluThrAlaAspAsnLysTyr 400
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QY 561 ArgProProLeuHisProAlaAspValProArgGlySerCysTyrGluThrAlaValGly 580
Db 1948 CGGCAACACACACCTCGAGATGTGCCAGAGGTTCTTCTGGGAGACAGCTGTGGGC 2007

| | | | |
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| QY | 581 | 11G1PHEMCAgLeuThrValSerAspMetLeuValThrTyrIleThrIleLeuLeu | 600 |
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| Db | 2008 | ATTTGATTTATGAGGCTCACCGCTGTGCAGATCGTGGTAATCACTCACCAATCTTGGCT | 2067 |
| QY | 601 | GLYAspPheLeuAlaGlyAsPheValArgPheMetValTyrCysTfPQsTfPAspLeu | 620 |
| | | | |
| Db | 2068 | GGAGATTTCCTCCAGGCTGTTTGTGTCCGGTTCAATGATCACTGCTGTTGGGACCTC | 2127 |
| QY | 621 | GLUAlaGlyPheProSerTyrAlaGluPheAspIleSerGlyAsnValIleGluGlyLeuIle | 640 |
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| Db | 2428 | TTTGACTGTGGCCCTTCAGTGGGAAAAAGAGATGACATGTCTCTCCATGGAGCAATC | 2487 |
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| Db | 2488 | GAGAGCAATTCCTTAAGTTTCGTGGGCAAGATCTTGTGCTCTCTGGCAACCAAGGCTG | 2547 |
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| QY | 781 | SerLeuSerAlaGlyAlaAsnAlaGlnLeuAlaGlyIysIysIleGlnValLeuAlaGlyValGlu | 800 |
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| QY | 841 | AlaSerGlnSerGlnIleAlaMetCAspIysIysAlaGlnIleYProGlyThrSerAsnSerAla | 860 |
| | | | |
| Db | 2788 | TTCAGGCAAAATCCAGACCTGGACAGAAAGGAGGAGGCCCCACACACTCGAGTCACTGAG | 2847 |
| QY | 861 | SerArgThrThrIleuProAlaSerGlyHisLeuProIleSerArgProProGlyIleGly | 880 |

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| Dp | 2305 | AAAGAAAGAAATGCATCGCACTGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGCAAC | 2364 |
| Qy | 810 | AlaThrAla-----ArgAspSerGluAspThrProlysSerSerSerLysAsnAlaThr | 827 |
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| Dp | 2365 | ACTAATTCAGATGCAAGATCTGGAGAGATTTACTTGCACGAAT----- | 2409 |
| Qy | 828 | GlnGluGlnLeuThrLysGlnGluThrThrProSerAlaSerGlnSerGlnAlaMet | 847 |
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| Qy | 848 | AspLysLysAlaGlnGlyProGlyThrSerAsnSerAlaSerArgThrThreLeuProAla | 867 |
| Dp | 2443 | GACACGAAAAAGATCTCTCC-----ATCAGACCAACCCCTGT----- | 2481 |
| Qy | 868 | SerCysHisLeuProIleSerArgProProGlyLysGlyProAspSerCysHisAlaPro | 887 |
| Dp | 2482 | ---GGAGAAACAGAAAA-AGCAGGAAGTCTGACACGACCCCAATAGCCCGTGGAGAAAG | 2537 |
| Qy | 888 | SerClnThrHisProTrpArgSerAlaSerGlyLysSerAlaGlnArgProPheHis | 906 |
| Dp | 2538 | AGCAGCATTCATCCACACACACACGACTGGTACACGGGCACTGACACGACGAC | 2594 |
| RESULT 4 | | | |
| AY581308 | | | |
| LOCUS | AY581308 | 2566 bp | mRNA linear VRT 31-MAY-2005 |
| DEFINITION | Gallus gallus transmembrane channel-like 1 (Tmc1) mRNA, complete cds. | | |
| ACCESSION | AY581308 | | |
| VERSION | AY581308.1 | GI:52547954 | |
| KEYWORDS | | | |
| SOURCE | Gallus gallus (chicken) | | |
| ORGANISM | Gallus gallus | | |
| | Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. | | |
| REFERENCE | 1 (bases 1 to 2566) | | |
| AUTHORS | Mutci,H., Mann,S. and Heller,S. | | |
| TITLE | Identification of Chicken Transmembrane Channel-Like (TMC) genes: Expression analysis in the cochlea | | |
| JOURNAL | Neuroscience 132 (4), 1115-1122 (2005) | | |
| REFERENCE | 15857715 | | |
| PUBMED | 2 (bases 1 to 2566) | | |
| AUTHORS | Mutci,H. and Heller,S. | | |
| JOURNAL | Direct Submission | | |
| | Submitted (24-MAR-2004) Otolaryngology, Harvard Medical School, Massachusetts Eye and Ear Infirmary, Eaton-Peabody Laboratory, 243 Charles Street, Boston, MA 02114, USA | | |
| FEATURES | | | |
| source | Location/Qualifiers | | |
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| | /db_xref="taxon:9031" | | |
| | /chromosome="2" | | |
| | /tissue_type="inner ear" | | |
| | /dev_stage="embryo" | | |
| | /note="breed: white leghorn" | | |
| gene | 1..2566 | | |

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Db 1324 GCTTCATCACTACCAAGCTTTAAAGAAAGCTCGTGAAGAGACAGAAAGCAAGAG 1383
QY 421 GluAsnIleHisLeuThrArgPheLeuArgValLeuValAsnPheLeuIleIleCysAsp 440
Db 1384 GAAATATTCTAGCTGCTCGGTCTGAAGGTTCTGTCAACTCTTAGGCTTCAGCA 1443
QY 441 LeuCysGlySerGlyTyrLeuIleTyrPheValValLysArgSerGlnGlnPheSer--- 459
Db 1444 CTTCGCTGGAGTGGCTACCTCATATTTTGTGTGTGAAGAAATCCCAAAATTTGCCCTG 1503
QY 460 ---LysMetGlnAsnValSerTyrTyrGluArgAsnGluValGluIleValMetSerLeu 478
Db 1504 GAAGCTCTGAAGAACTACGGGTGGTGGAAAGAAATGAAGTAAATGATGTCATGTCACCT 1563
QY 479 LeuGlyMetPheCysProIleLeuPheGluThrIleValLeuGluAsnTyrHisPro 498
Db 1564 TTGGGATGTTCTGTCAACCTGTTTGATGTTATCACTTCGGAAGAACTAACATCTCT 1623
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QY 519 ThrPheLeuLeuValLeuMetCaspAspValHisLeuLysLeuValAsnGluGluThrIle 538
Db 1684 ACTTCATATTGCTCATATGATGAATCAATCTCAAGTTCGAAAGAAAGATATCTC 1743
QY 539 Lys---AsnIleThrHisTyrThrLeuPheAsnTyrTyrAsnSerSerGlyTyrAsnGlu 557
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QY 558 SerValProArgProIleuHisProAlaAspValProArgLysCysTyrPqlnThr 577
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QY 578 AlaValGlyIleGluPheMetCArgLeuThrValSerAspMetLeuValThrTyrIleThr 597
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QY 598 IleLeuLeuGlyAspPheLeuArgAlaCysPheValArgPheMetAsnTyrCysTyrPro 617
Db 1924 ATTCTAATTGGTGACTTCTGAGAGCTGCTTTGTGTAGGTTTTCATTTACTGCTGGTGC 1983
QY 618 TrpAspLeuGluValaGlyPheProSerTyrAlaGluPheAspIleSerGlyAsnValLeu 637
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QY 718 ProProSerPheAspCysGlyProPheSerGlyLysAsnArgPheCtyrAspValLeuGln 737
Db 2284 CACCATCTTTTGAAGTGGCCCTTCAAGCGGAAACAAAGATGTTGAAGTCATATCA 2343
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Job time : 10113 secs

OM protein - nucleic search, using frame_plus_p2n model
Run on: December 4, 2005, 17:37:51 ; Search time 1128 Seconds
(without alignments)
5353.024 Million cell updates/sec

Title: US-10-792-307-4
Perfect score: 4744
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Scoring table:
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-OUTFMT=pcr -NOR-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
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- 12: geneseqn2004as:*
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- 14: geneseqn2005as:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 4642 | 97.8 | 3121 | 8 | ACCG69614 Human tra |
| 2 | 4325.5 | 91.2 | 5027 | 5 | AA5922296 DNA encod |
| 3 | 3808 | 80.3 | 3216 | 8 | ACCG69616 Mouse tra |
| 4 | 2344.5 | 49.4 | 4333 | 8 | ACCG69613 Human tra |
| 5 | 2300 | 48.5 | 2895 | 8 | ACCG69615 Mouse tra |
| 6 | 1619 | 34.1 | 3357 | 13 | ADU01837 Human tra |
| 7 | 1466 | 30.9 | 2560 | 11 | ADM01657 Human tra |
| 8 | 1456.5 | 30.7 | 3897 | 13 | ADU01668 Human tra |
| 9 | 1227 | 25.9 | 2591 | 6 | ABV75613 Human tra |
| 10 | 1120.5 | 23.6 | 5929 | 4 | ABU05865 Human tra |
| 11 | 679 | 14.3 | 2758 | 11 | ADM01585 Human tra |
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| c 14 | 517.5 | 10.9 | 2358 | 11 | ACN92177 Breast ca |
| 15 | 516 | 10.9 | 2355 | 6 | ABZ23382 Nucleotid |
| c 16 | 516 | 10.9 | 2355 | 6 | ABZ23383 Reverse c |
| 17 | 515 | 10.9 | 2403 | 4 | AAFG1776 Human mem |
| 18 | 499.3 | 10.3 | 2321 | 3 | AAAI6626 Human sec |
| c 19 | 493 | 10.4 | 11963 | 4 | ABU05864 Drosophi1 |
| 20 | 486 | 10.2 | 2001 | 6 | ABZ11813 Human pol |
| 21 | 486 | 10.2 | 2001 | 12 | ADM44331 Novel hum |
| 22 | 473.5 | 10.0 | 2824 | 14 | ADY17129 DNA encod |
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| 24 | 465.5 | 9.8 | 4572 | 10 | ADD69632 Human REM |
| 25 | 457.5 | 9.6 | 2902 | 6 | ABQ54905 Human ova |
| 26 | 449.5 | 9.5 | 2359 | 11 | ADM03417 Human cDN |
| 27 | 449.5 | 9.5 | 3256 | 9 | ACC48561 Transmemb |
| 28 | 449.5 | 9.5 | 3285 | 11 | ADN39832 Cancer/an |
| 29 | 449 | 9.5 | 3666 | 9 | ADA09906 Human rec |
| 30 | 447.5 | 9.4 | 2203 | 10 | ADP95581 Human NOV |
| 31 | 446 | 9.4 | 2433 | 12 | ADG67421 Human NOV |
| 32 | 442 | 9.3 | 2418 | 8 | ACC48786 Human Evi1 |
| 33 | 442 | 9.3 | 2420 | 8 | ACC48790 Human Evi1 |
| 34 | 442 | 9.3 | 2420 | 8 | ACC48791 Human Evi1 |
| 35 | 439.5 | 9.2 | 3812 | 10 | ADJ21979 Novel1 hum |
| 36 | 437.5 | 9.2 | 2389 | 8 | ACC48788 Human Evi1 |
| 37 | 434 | 9.1 | 2057 | 10 | ADJ21987 Novel1 hum |
| 38 | 428.5 | 9.0 | 1839 | 14 | AEBS5641 Human pol |
| 39 | 428.5 | 9.0 | 2389 | 8 | ACC48792 Human Evi1 |
| 40 | 422.5 | 8.9 | 2421 | 9 | ACC48570 TMOC part |
| 41 | 418 | 8.8 | 5357 | 12 | ADD86636 Human tra |
| 42 | 355 | 7.5 | 2131 | 9 | ACC59891 Human REM |
| 43 | 338 | 7.1 | 1804 | 13 | ADP23695 PPO polyp |
| 44 | 338 | 7.1 | 1804 | 13 | ADU06103 Novel1 bro |

ALIGNMENTS

RESULT 1

ACCG69614
ID ACCG69614 standard; cDNA; 3121 BP.

ACCG69614;

DT 18-JUL-2003 (first entry)

XX Human transductin-2 (TDC2) encoding cDNA SEQ ID NO:3.

KW Human; transductin-2; TDC2; hearing loss; auditory; gene therapy; gene;

XX ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS

FT /'tag' = a
/product= "transductin-2"

XX MO2003025140-A2.

XX 27-MAR-2003.

XX 19-SEP-2002; 2002MO-US029614.

XX 19-SEP-2001; 2001US-0323275P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Griffith AJ, Kurima K, Wilcox E, Friedman T;

XX WPI; 2003-371806/35.

XX P-PSDB; ABR43616.

XX An isolated or purified nucleic acid molecule encoding transductin-1

XX (TDC1), TDC2, or its fragment, useful for prognosticating, treating or

XX Claim 9; Fig 2; 85pp; English.

XX The present sequence encodes human transductin-2 (TDC2). The present

XX invention describes human and mouse TDC1 and TDC2. Also described: (1) a

XX method for detecting hearing loss or predisposition to hearing loss in an

XX animal; (2) a method for determining the level of nucleic acid comprising

XX wild-type TDC1 or TDC2 gene and/or mutant TDC1 or TDC2 gene in a test

XX sample comprising a nucleic acid comprising the wild-type TDC1 or TDC2

XX gene and/or mutant TDC1 or TDC2 gene obtained from the animal; (3) a

XX method for detecting the level of wild-type TDC1 or TDC2, and/or mutant

XX TDC1 or TDC2 in a test sample comprising a protein comprising the wild-

XX type TDC1 or TDC2 gene and/or mutant TDC1 or TDC2 gene in a test sample

XX comprising a nucleic acid comprising the wild-type TDC1 or TDC2 gene

CC and/or mutant TDC1 or TDC2 gene obtained from the animal); (4) a method
 CC for treating an animal prophylactically or therapeutically for hearing
 CC loss due to a complete or partial loss of wild type TDC1 or TDC2; and (5)
 CC a method for identifying one or more agents that interact with a TDC1
 CC and/or TDC2 genes in a cell by administering one or more agents to the
 CC cell comprising the genes and assaying the expression level of the genes
 CC by the cell, where an increase or decrease in the expression level is
 CC indicative of the interaction between the agents and the genes in the
 CC cell. TDC1 and TDC2 have auditory activities and can be used in gene
 CC therapy. The molecules, compositions and methods of the present invention
 CC can be used for prognosticating, treating and monitoring hearing loss

SQ Sequence 3121 BP; 778 A; 823 C; 824 G; 696 T; 0 U; 0 Other;

Alignment Scores:

| | | | |
|------------------------|---------|---------------|------|
| Pred. No.: | 0 | Length: | 3121 |
| Score: | 4642.00 | Matches: | 890 |
| Percent Similarity: | 98.23% | Conservative: | 0 |
| Best Local Similarity: | 98.23% | Mismatches: | 0 |
| Query Match: | 97.85% | Indels: | 16 |
| DB: | 8 | Gaps: | 1 |

US-10-792-307-4 (1-906) x ACCG69614 (1-3121)

QY 1 MetSerHisGlnValIysGlyLeuIysGlnGluAlaArgGlyValIysGlyArgVal 20

DB 16 ATGAGCCACCAAGGTAAAGGCTGAAAGAGAA-----

QY 21 LysSerGlySerProHisThrGlyAspArgLeuGlyArgArgSerSerLysArgAla 40

DB 49 -----GGTGAAGGCTGGGAAGGAGATCTCAAGACAAAGCGGCT 87

QY 41 LeuLysAlaGluGlyThrProGlyArgArgGlyAlaGlnArgSerGlnLysGluArgAla 60

DB 88 CTCAAAGCCAGAGGAGACCCAGGAGGCGGAGCTCAGCAGAACCAAGAGAGCGGCGC 147

QY 61 GlyGlySerProSerProGlySerProArgArgGlnThrGlyArgArgHisArg 80

DB 148 GGGGGAGCCCAAGCCCGGGGTCTCCCGGAGAAACAAGGGGCGAGAGACACAGA 207

QY 81 GluGluLeuGlyGluGlnGluArgGlyGluAlaGluArgThrCysGluGlyArgArgLys 100

DB 208 GAAGAGCTGGGGGAGCAGAGAGCGGGCGAGAGAGAGACTCTCCAGGCGAGAGAAAG 267

QY 101 ArgAspGluArgAlaSerPheGlnGluArgThrAlaAlaProLysArgGluLysGluIle 120

DB 268 CCGAGCAGAGAGGGGCTCTTCCAGAGCGGAGAGCCCAAGAGGAAAGAGAGATT 327

QY 121 ProArgGlyGluGluLysSerLysArgGlnLysLysProArgSerSerLeuAlaSer 140

DB 328 CCGAGGAAAGAGAGAGTGAAGGCGCAGAAACCAAGTCACTCTTGGCTCC 387

QY 141 SerAlaSerGlyGlyLysSerLeuSerGluGluLeuAlaGlnIleLeuGluGlnVal 160

DB 388 AGTGGCTCTGGGGAGATCCCTGTCAGAGAGAAAGTGGCCCAAGTCTTGGACAGAGTG 447

QY 161 GluGluLysLysLysLeuIleAlaThrMetArgSerLysProTrpProMetAlaLysLys 180

| | | | | | | | |
|----|------|--|------|--|------|---|------|
| Db | 448 | GAAGAAAAAGAAAGCTCAATTCACCAATCGGAGCAAGCCCTGGCCCATGGGAGAAAG | 507 | | 1288 | TTGTGTGSAAGTGGGTACCTCAATTACTTTGTGGTTAAAGCAATCTCAGCAATTCACAA | 1347 |
| QY | 181 | LeuThrGluLeuArgGluAlaGlnGluPheValGluValTyrGluGlnValAlaLeuGlyLys | 200 | | 461 | MetGlnAsnValSerTyrTyrGluArgAsnGluValGluValLeuValMetSerLeuLeuGly | 480 |
| Db | 508 | CTGACAGAGCTCAGGGAGGCCAGGAATTTGGAGAGATGAAGGTCCTTGGGAAG | 567 | | 1348 | ATGCAGAAATGTCAGGCTGGTATGAAGAGATGAGATGAGATGCTGATGCTGCTTGGCA | 1407 |
| QY | 201 | GlyLysGlyLysGlnLeuTyrAlaTyrLysMetLeuMetAlaLysLysTyrValLysPhe | 220 | | 481 | MetPheCysProProlLeuPheGluThrLLeuAlaAlaLeuGluAsnTyrThrAspProArgThr | 500 |
| Db | 568 | GGGAAAGGCAAGCACTATATCCCTACAAAGATGCTGATGGCCAGAAATGGGTCAAATTT | 627 | | 1408 | ATGTTTGTCCCTCTGTGTTGAACCATGCGTGGCTGGAGAAATTAACCAACCGCATTT | 1467 |
| QY | 221 | LysArgAspPheAspAsnPheLysThrGlnCysIleProTyrGluMetCysIleLysAsp | 240 | | 501 | GlyLeuLysTyrProlLeuGluYahGlyIlePheAlaLeuPheLeuGluAsnLeuTyrThrPhe | 520 |
| Db | 628 | AAAGACAGCTTTCATTAATTCAGACCTCAATGTATCCCTGGGAAATGAAGATCAAGGAC | 687 | | 1468 | GACCTGAAGTGGACCTGGAGGACATCTTGGCACTCTCTGGGAAACCTCTACACATTT | 1527 |
| QY | 241 | IleGluSerHisPheGlySerSerValAlaSerTyrPheAlaPheLeuAlaGlyTyrPheCys | 260 | | 521 | LeuLeuAlaLeuMetCysAspAspValHisLeuLysLeuValLeuAlaAsnGluGluThrIleLysAsn | 540 |
| Db | 688 | ATTGAAGTCACTTTGGTTCTTCAGTGGCATCGTATTTCAATCTTTCTCCGATGGATGTAT | 747 | | 1528 | CTCTTGGCCCTGATGGATGACGTCCACCTCAAGCTTGCTGAATGAAGAACAATAAGAAC | 1587 |
| QY | 261 | GlyValAsnLeuValLeuPheGlyLeuAlaPheGlyLeuValIleIleProGluValLeu | 280 | | 541 | IleThrHisTyrThrLeuPheAsnTyrTyrAsnSerSerGlyTyrAsnGluSerValPro | 560 |
| Db | 748 | GGAGTTAACTGTGCTTTTGGCTAATATTTGGTCTAGTCATATCCAGAGGTACTG | 807 | | 1588 | ATCACTCAGTGAAGCTGTGTTAACTATTACAACTCTTCTGGTTGGAAACGAGGTCTCCC | 1647 |
| QY | 281 | MetGlyMetProTyrGlySerIleProArgLysThrValProArgAlaGluGluGluLys | 300 | | 561 | ArgProProlLeuHisProAlaAspValProArgLysSerCysTyrProlThrAlaValGly | 580 |
| Db | 808 | ATGGGCATGCCCTATGGAGATATCCAGAAAGACAGTGCCTCGGGCTGAGAAAGAAAG | 867 | | 1648 | CAACCAACCCCTGCACCCCTGCAGATGTGCCCGGAGTTCTCTGGGAGACAGCTGTGGAC | 1707 |
| QY | 301 | AlaMetCysPheSerValLeuThrPhePheGluGlyTyrIleLysTyrSerAlaLeuPhe | 320 | | 581 | IleGluPheMetCysArgLeuThrValSerAspMetLeuValThrTyrIleThrIleLeuLeu | 600 |
| Db | 868 | GCATGGATTTTCTGTCTTTGGGATTTTGAAGGCTATATCAAGTACTCTGCACCTCTTC | 927 | | 1708 | ATTGAATTCAATGAGGCTGACGGTGTGACATGCTGTGATGATGATCAACATCTCTGCG | 1767 |
| QY | 321 | TyrGlyTyrTyrAsnAsnGlnArgThrIleGlyTyrPheLysArgTyrArgLeuProMetAla | 340 | | 601 | GlyAspPheLeuArgAlaCysPheValArgPheMetCysAsnTyrCysTyrProCysTyrAspLeu | 620 |
| Db | 928 | TATGGCTACTACAAACAACAGAGAACATCGGGTGGGTGAGGTACCGGCTGGCTATGGCT | 987 | | 1768 | GGGAGCTTCCCTACGGGCTGTGTTTGTGGGGTTCATGAAGTACTGTGGTGGTGGGACTTG | 1827 |
| QY | 341 | TyrPheMetCysAlaGlyAlaSerValPheGlyTyrSerLeuIleIleValIleArgSerMet | 360 | | 621 | GluAlaGlyPheArgProSerTyrAlaGluPheAspIleAsnGlyAsnValLeuGlyLeuIle | 640 |
| Db | 988 | TACTTTATGGTGGGGGTCAAGGCTGTGGCTACAGCCTGATTTATGTCATTCGATCGATG | 1047 | | 1828 | GAAGCTGAATTTCTCTCATATGCTGAGTTGATATTAGGAAATGTGCTGGGTTTGATC | 1887 |
| QY | 361 | AlaSerAsnThrGlnGlySerThrGlyGluGlyGluSerAspAsnPheThrPheSerPhe | 380 | | 641 | PheAsnGlnGlyMetIleTyrPheGlySerPheTyrAlaProGlyLeuValGlyIleAsn | 660 |
| Db | 1048 | GCCAGCAATACCCAGAAAGCAGCGGAAAGGGAAGTGACAACTTCACATTCAGCTTC | 1107 | | 1888 | TTCAACCAAGAAATGATCTGAGATGGGCTCCTCTCATATGCTCCAGGCGCTGGTGGCATTTAAT | 1947 |
| QY | 381 | LysMetPheThrSerTyrAspTyrLeuIleGlyAsnSerGluThrAlaAspAsnLysTyr | 400 | | 661 | ValLeuArgLeuLeuThrSerMetTyrPheGlnCysTyrPylAlaValMetSerSerAsnVal | 680 |
| Db | 1108 | AAAGATGTTCAACAGCTGGGACTACCTGATCGGGAAATTCAGAGACACGCTGATTAACAAATAT | 1167 | | 1948 | GTGCTGGGCTGCTGACCTCCATGTACTTCAGTGTGCTGGGCGGTGATGAAGCAACGTAA | 2007 |
| QY | 401 | AlaSerIleThrThrSerPheLysGluSerIleValAspGluGlnGluSerAsnLysGlu | 420 | | 681 | ProHisGluArgValPheLysAlaSerArgSerAsnAsnPheTyrPheGlyLeuLeuLeu | 700 |
| Db | 1168 | GCATCCATCAACAACGCTTCAGGAATCAATAGTGGATGAACAAAGAGGTAAACAAAGAA | 1227 | | 2008 | CCCATGAACGGCTGTCCAAAGGCTCCCGATCCAAACACTTCATCATGGGCTCTGCTG | 2067 |
| QY | 421 | GluAsnIleHisLeuThrArgPheLeuArgValLeuValAsnPheLeuIleIleCysCys | 440 | | 701 | LeuValLeuPheLeuSerLeuLeuProValAlaTyrThrIleMetSerLeuProProSer | 720 |
| Db | 1228 | GAAATATATCATCTGACAAGATTTCTTGCTGTCTGGCAACTTCTCATCATCTGCTGT | 1287 | | 2068 | CTGGGTCTTTCCTCAGGCTCCGTCGGGTGGCTACACATCATGTCCTGCCACCGCTCG | 2127 |
| QY | 441 | LeuCysGlySerGlyTyrLeuIleTyrPheValValLysArgSerGlnGlnPheSerLys | 460 | | 721 | PheAspCysGlyTyrProPheSerGlyLysAsnArgMetTyrAspValLeuGlnGluThrIle | 740 |
| | | | | | 2128 | TTTGACTGCGGGCGCTTCACTGGGAAAAACAGATGTACGATGTCTCCAAAGAACCATTT | 2187 |

QY 741 GluAsnAspPheProThrPheLeuGlyLysIlePheAlaPheLeuAlaAsnProGlyLeu 760
D 2188 GAAACGATTCACCACTTCCTGGCAAGATCTTTCCTTCCTGGCAATCCAGGCTG 2247
QY 761 IleIleProAlaIleLeuLeuPheLeuAlaIleTyrTyrLeuAsnSerValSerLys 780
D 2248 ATCATCCAGGCATCCTGCTGATGTCTTGGGCATTTACCTGAACTGAACTGATTCGAAA 2307
QY 781 SerLeuSerArgAlaAsnAlaGlnLeuArgLysLysIleGlnValLeuArgLysValGlu 800
D 2308 AGCCTTCCGAGCTAATGCCAGCTGAGGAAAGAAATCCAAAGTCTCCCTGAAGTTGAG 2367
QY 801 LysSerHisLysSerValLysGlyLysAlaThrAlaArgAspSerGluAspThrProLys 820
D 2368 AAGAGTCACAAATCTGTAAAGGCCAAAGCCAGCCAGATTCAGAGGACACACTTAAA 2427
QY 821 SerSerSerLysAsnAlaThrGlnLeuGlnLeuThrLysGluGluThrThrProProSer 840
D 2428 AGCAAGCTCAAAAATGCCAGCAAGCTCCAACTCAACAAAGAAAGAACCACTCCCTCT 2487
QY 841 AlaSerGlnSerGlnAlaIleAspLysLysAlaGlnGlyProGlyThrSerAsnSerAla 860
D 2488 GCCAGCCAAAGCCAGCCATGACAAAGAGGCCGCGGACCTCGGACCTCAATCTGCC 2547
QY 861 SerArgThrThrLeuProAlaSerGlyHisLeuProIleSerArgProProGlyTleGly 880
D 2548 AGCAGGACCACTGCTGCTCTGGACACCTTCTATATCTCGGCCCTCGAATCGGA 2607
QY 881 ProAspSerGlyHisAlaProSerGlnThrHisProTyrArgSerAlaSerGlyLysSer 900
D 2608 CCAGATTCGGCCAGCCCCCATCTCAAGACTCATCCGTGAGGTCAAGCTCTGAAAGAGT 2667
QY 901 AlaGlnArgProProHis 906
D 2668 GCTCAGAGACCTCCAC 2685

RESULT 2
AAS92296
ID AAS92296 standard; cDNA; 5027 BP.
AC AAS92296;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #28100.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN W0200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
PI Dzmanec RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; AB628109.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 28100; 103bp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantifying a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 5027 BP; 1316 A; 1289 C; 1339 G; 1083 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.85e-295 Length: 5027
Score: 4325.50 Matches: 843
Percent Similarity: 89.70% Conservative: 10
Best Local Similarity: 88.64% Mismatches: 17
Query Match: 91.18% Indels: 61
DB: Gaps: 5

US-10-792-307-4 (1-906) x AAS92296 (1-5027)

QY 22 SerGlySerProHis-----ThrGlyAspArgLeuGlyArgArgSerSerLysArg 39
D 25 GCTGCTCGAAGCACTGACCTCAGGTGACAGGCTGGGAGAGAGATCCCTCAAGCAAGCGG 84
QY 40 AlaLeuLysAlaGlnGlyThrProGlyArgArgGlyAlaGlnArgSerGlnLysGluArg 59

| | | | | | | | | |
|----|------|---|------|--|----|------|---|------|
| Ds | 85 | GCTCTAAAGCCAGGGGACCCAGCAGGCGCGAGCTCAGAGAAAGCCAGAAAGAGCGC | 144 | | Ds | 904 | TGCTACGGTCTAGGTTTGAACAAAGGCTACAAATTACTTGAAGCGGTAGACTGAAGAGATC | 965 |
| Qy | 60 | AlAGlyIySeRProSeRProGlySeRProARgLySGlnThRgLyARgARgHIs | 79 | | Qy | 305 | ----- | 305 |
| Ds | 145 | GCGGGGGGACCCCAAGCCGGGGGCTCCCGAGAGAAACAAGGGGCGCAGAGACAC | 204 | | Ds | 964 | CGCTTCAGAGCTCACTCAGATGGCTACTGGAGACTCAGAGATACAAATTTCAAGCTTA | 1023 |
| Qy | 80 | ArgGluGluwauGlyGluGlnGlyGlyGlywAlaGlywRgThCyGlyGlywLyARgRg | 99 | | Qy | 306 | ValLeuITrp----- | 308 |
| Ds | 205 | AGAGAAAGAGCTGGGGGAGAGAGCGGGGGCGAGGCGAGAGAGAGCTGGGAGGGCGAGGA | 264 | | Ds | 1024 | CTCAGGTGGCTTCTGGCAGGGCTCAGAAAATCTGCTCCAACTTACTTATGTGGCTGTT | 1083 |
| Qy | 100 | LyARgAspGlywARgAlaSeRPhelGlnGlywARgThAlaAlaProLySARgGlywGlyu | 119 | | Qy | 309 | ---AspPhelGlyuLyTrIleLySARgAlaLeuPhelYrGlyTrTyARgAsnGln | 327 |
| Ds | 265 | AAGCGGAGAGAGGGGCGCTCTTCAGAGAGCGCAGACAGACCCCAAGAGGAAAAAGAG | 324 | | Ds | 1084 | CCCAAGGTCAAGGGCTATACAAAGTACTGCACTCTCTATGGCTACTACAAACACAG | 1143 |
| Qy | 120 | ILeProARgLyGlnGlywLySeRLySARgGlnLySARProARgSeRSeRLeuAla | 139 | | Qy | 328 | ArgThTrIleGlyTrPhLeuARgYrARgLeuProARgAlaYrPhelwARgLyAlaSeR | 347 |
| Ds | 325 | ATTCCAGAGAGAGGAGAGAGTCCAGACGGCAGAAACCCAGGTCTACTCTCTTGGCC | 384 | | Ds | 1144 | AGAGCCATCGGGGCTGAGGATCGGGCTGCTATGGCTTCTTATGGTGGGGCTACG | 1203 |
| Qy | 140 | SeSeRAlaSeRGIyGlyGlyuSeRLeuSeRGIyGlnGlyuLeuAlaGlnILeLeuGln | 159 | | Qy | 348 | ValPhelGlyTrSeRLeuILeILeAlaILeARgSeMeAlaSeRAnThRgInGlySeR | 367 |
| Ds | 335 | TCCAGTGGCTCTGGTGGGAGTCCCTGTCCAGAGAGAGACTGGCCCGGATCTCGAGAG | 444 | | Ds | 1204 | GTGTTCGGCTACAGGCTGATATTGTCAATGCATGCATGGCAGCAATCCCAAGAGAGC | 1263 |
| Qy | 160 | ValGlnGlyLyLySARLeuILeAlaThRgARgSeRLySARProARgProARgAlaLyS | 179 | | Qy | 368 | ThRgLyGlyGlyuSeRAspAnPhelThRheSeRPhelywARgThSeRTrpAsp | 387 |
| Ds | 445 | GTGGAAAGAAAAAGAAAGCTCATTGCCACCATGGGAGCAAGCCCTGGCCCATGGCGAG | 504 | | Ds | 1264 | ACAGCGAAAGGAGAGAGCAACTTCACTCACTCAAGCTCAAGAGTTCCACACGCTGGGAC | 1323 |
| Qy | 180 | LyLeuThRgLywLeuARgLywAlaGlnGlywPhelAlaGlywLyTrGlnGlyAlaLeuLy | 199 | | Qy | 388 | TrLeuILeGlywAnSeRGIyThRAlaAspAnLySARAlaSeRILeThRSeRPh | 407 |
| Ds | 505 | AAGCTGACAGAGCTCAGGGAGGCGACAGAAATTTGTGAGAGAGTATGAAGCGCGCTTGGGA | 564 | | Ds | 1324 | TACTGATCGGGAATTCAGAGAGCGTATACAAATATGATCATCAACCAACGAGCTTC | 1383 |
| Qy | 200 | LyGlyLySARGIyGlnGlyuLyARLeTyRLywARLeuMeARLeAlaLySTPwLyLyS | 219 | | Qy | 408 | LyGlyuSeRILeAlaAspGlnGlnGlyuSeRAnLySGLuGlyuAnILeILeAlaThARg | 427 |
| Ds | 565 | AAGGGAAAGGCAAGCACTAATGCTACAAAGATGCTATGGCCAGAAATGGGTCAA | 624 | | Ds | 1384 | AAGGATCAATATGGATGAAACAAGAGATACAAAGAAAGAAATATCCATCTGACAGA | 1443 |
| Qy | 220 | PhelywARgAspARgAspAnPhelyThRgCySILeProTRpGlywARgLyLyS | 239 | | Qy | 428 | PhelwARgYAlaLeuAlaAnPhelLeuILeILeCySLeuCySGLySeRGIyTrLeu | 447 |
| Ds | 625 | TTTAAAGAGACTTGTATATTTCAGAGCTCAATGTATCCCTGGGAAATGAAGATCAA | 684 | | Ds | 1444 | TTTCTTGCTGTCGGCCCACTTCTCACTCATGCTGTTGTGTGGAGTGAACCTC | 1503 |
| Qy | 240 | AspILeGlyuSeRILePhelGlySeRSeRValAlaSeRTrPhelLeuPhelwARgTRpAR | 259 | | Qy | 448 | ILeTrPhelValLyAlaARgSeRGIyPhelSeRLySMeRGIyAnLySeRTPYR | 467 |
| Ds | 665 | GACATTTGAAATCATCTTGGTCTTCAGTGGCATCGATATTCATCTTCTCCAGTGAATG | 744 | | Ds | 1504 | ATTACTTGTGGTTAAAGCATTCAGCAATCTCAAAATGCAAGATTCAGCTGGTAT | 1563 |
| Qy | 260 | TrGlyLyAlaAnLeuValLeuPhelGlyLeuILePhelGlyLeuAlILeILeProGlyuAl | 279 | | Qy | 468 | GlywARgAnGlyuAlaGlyuILeAlaMeSeRLeuGlywARgPhelCySARProLeuPho | 487 |
| Ds | 745 | TATGAGTTAACCTTGCTGCTTTTGGCTTAATATTGTGCTAGTCAATATCCAGAGGAT | 804 | | Ds | 1564 | GAAGAAATAGAGTGAAGATCGATGTGCTGCTGAGATGTTGTGCCCTCTGTT | 1623 |
| Qy | 280 | LeuMeARgLywARgPro----- | 299 | | Qy | 488 | GlywThRILeAlaLeuGlywAnTyRILeProARgThRgLywLySTrPGLnGlyu | 507 |
| Ds | 805 | GTCTACGTGAACCTCGAGAAACCTCAATTAGCTCAGAGAGCTGGCGCAAGGCGCCA | 864 | | Ds | 1624 | GAAGCCATCGCTGCCCTCGAGAAATTAACACCAAGCACTGAGCTGAAGGTGAGACTGGGA | 1683 |
| Qy | 290 | ARgLyThRValIProARgAlaGlyGlyuGlyuSARLeuARgPhSeSeR----- | 305 | | Qy | 508 | ARgILePhelAlaLeuPhelGlyuGlyuAnLeuTrThRPhelLeuAlaLeuMeARpAsp | 527 |
| Ds | 865 | CTG-----GATGACAAAGTTATGTACTTCTCTCAACACGTGGA | 903 | | Ds | 1684 | CGCATCTTTCAGCTCTCTCGGGAAAGCTGACACATTTTCCTTGGCCCTGAGATGAC | 1743 |
| Qy | 305 | ----- | 305 | | Qy | 528 | ValHISLeuLySARLeuAlaAnGlyuThRILeLySAnILeThRILeSTrPThLeuPho | 547 |
| Ds | 1744 | GTCCAGCTCAAGCTTGCTGATATGAAGAGCAATAAAGAACTCACTCACTGAGCTCTGTT | 1803 | | Ds | 1744 | GTCCAGCTCAAGCTTGCTGATATGAAGAGCAATAAAGAACTCACTCACTGAGCTCTGTT | 1803 |

QY 548 AantYrTYrAsnSerSerGlyTrpAangIuseValProArpProProLeuHisProAla 567
 |||||
 Db 1804 AACTATTAGCACTCTTGGTTGGAAAGAGAGTGTCCCCGACCAACCCCTGCACCCCTGCA 1863
 QY 568 AaspValProArGlySerCyatTrpGluThrAlaValGlyIleGluPheLeuThr 587
 |||||
 Db 1864 GATGTGCCCGGGGTCTTGGTGGGAGACAGCTGTGGGCATTGAATTCAATGAGGCTGACC 1923
 QY 588 ValSerAspPheLeuValThrTyrlleThrIleLeuLeuGlyAspPheLeuArgAlaCys 607
 |||||
 Db 1924 GTGTCTGACATGCTGGTAACGTACATCAACCATCCTGCTGGGGAGCTTCTACAGGCTTGT 1983
 QY 608 PheValArGpPheLeuAsnTyrcystrpCystrpAspLeuGluValaglPheProSerTyrc 627
 |||||
 Db 1984 TTTGTGGGTTCAATGAAGTACTGCTGTGTGGGACTGTGGAGCGGTGATTTCTTCATAT 2043
 QY 628 AlaGluPheAspIleSerGlyAsnValLeuGlyLeuIlePheAsnGlnGlyHetiIleTrp 647
 |||||
 Db 2044 GCTGAGTTGATTATGAGGAAATGTCTGGGTTTGAATCTTCACCAAGGAATGATCTGG 2103
 QY 648 MetGlySerPheTrpAlaProGlyLeuValGlyIleAsnValLeuArGLeuLeuThrSer 667
 |||||
 Db 2104 ATGGGCTCCTTCTATGCTCCAGGCTGTGGCATTAATGTCTGGCCTGCTGACCTCC 2163
 QY 668 MetTyrcPheGlnCystrpAlaValIleMetSerSerAsnValProHisGluArgValPheLys 687
 |||||
 Db 2164 ATGTACTTCCAGTGGTGGGCGGTGATGACAGCAAGTACCCCATGAACCGGTGTTCAA 2223
 QY 688 AlaSerArGSerAsnAsnPheTyrcGlyLeuLeuLeuLeuValLeuPheLeuSerLeu 707
 |||||
 Db 2224 GCCTCCGATCCAAACAATCTTCAATGGGCTCCTGCTGTGTGCTTCTCTCAGCCTC 2283
 QY 708 LeuProValAlaTyrcThrIleMetSerLeuProProSerPheAspCysGlyProPheSer 727
 |||||
 Db 2284 CTGGCGGTGGCTACACCATCATGTCCCTCCACCCCTCCTTGACTGGGGCGGTCACT 2343
 QY 728 GlyLysAsnArGHeTyrcAspValLeuGlnGluThrIleGluAsnAspPheProThrPhe 747
 |||||
 Db 2344 GGGAAAAACGAATGTACGATGTCTCCAAAGACCATTGAAAAAGATTCCCAACCTTC 2403
 QY 748 LeuGlyLysIlePheAlaPheLeuAlaAsnProGlyLeuIleIleProAlaIleLeuLeu 767
 |||||
 Db 2404 CTGGCAAGATCTTGTCTTCTCTGCAATCCAGGCTGATCATCCAGCAATCCTGCTG 2463
 QY 768 MetPheLeuAlaIleTyrcTyrcLeuAsnSerValSerLysSerLeuSerArGAlaAsnAla 787
 |||||
 Db 2464 ATGTCTTGGCATTTACTACTGAATCAATTCAGTTCCAAAAAGCCTTCCGAGCTAATGCC 2523
 QY 788 GlnLeuArGlyLysIleGlnValLeuArGluValGluLysSerHisLysSerValLys 807
 |||||
 Db 2524 CAGCTGAGGAAGAAATCCAAAGTGTCCGTCAAGTTGAGAAAGAGTCAAAATCTGTAAA 2583
 QY 808 GlyLysAlaThrAlaArgAspSerGluAspThrProLysSerSerSerLysAsnAlaThr 827
 |||||
 Db 2584 GGGAAAGCCACAGCCAGATTCCAGAGACACCTAAAGAGCTCAAAAAATGCCACC 2643

QY 828 GlnLeuGlnLeuThrLysGluGluThrThrProProSerAlaSerGlnSerGlnAlaMet 847
 |||||
 Db 2644 CAGCTCCAACTCACCAAGGAAGAGACCACTCTCCCTCTGCCAGCCAAAGCCAGGCCATG 2703
 QY 848 AspLysIleValGlnGlyProGlyLysSerAsnSerAlaSerArGThrThrLeuProAla 867
 |||||
 Db 2704 GACAAAGAGGCGAGGGCCCTGGGACCTCCAAATTCGCCACAGACCAACTGCTGCTGCC 2763
 QY 868 SerGlyHisLeuProIleSerArGProProGlyIleGlyProAspSerGlyHisAlaPro 887
 |||||
 Db 2764 TCTGGACACTTCTCATATCTGGGCCCTGGAAATCGACAGATTCTGGCCACGCCCA 2823
 QY 888 SerGlnThrHisProTrpArGSerAlaSerGly 898
 |||||
 Db 2824 TCTCAGACTCATCCCTGGAGACAGGGGCTGGG 2856

Search completed: December 4, 2005, 20:52:13
 Job time : 1226 secs

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 17:37:51 ; Search time 392 Seconds
(without alignments)
4215.892 Million cell updates/sec

Title: US-10-792-307-4
Perfect score: 4744
Sequence: 1 MSHQVKGLEKKEARGVKGRV.....PSQTHPMWSASGSKAQRPPH 906

Scoring table:

| | |
|---------------------------|--|
| BLOSUM62 | |
| Xgapop 10.0 , Xgapext 0.5 | |
| Ygapop 10.0 , Ygapext 0.5 | |
| Egapop 6.0 , Egapext 7.0 | |
| Delop 6.0 , Delext 7.0 | |

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xip
-O/cgn2_1/USPTO_spool_p/US10792307/runet_23112005_080713_19195/app_query.fasta_1
-1095
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=tblsum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORW=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10792307 @CGN 1.1 290 @runet_23112005_080713_19195 -ICPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DISPATCH=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_NA:*

- 1: /cgn2_6/ptodate/1/lna/1.COMB.seq:*
- 2: /cgn2_6/ptodate/1/lna/5.COMB.seq:*
- 3: /cgn2_6/ptodate/1/lna/6A.COMB.seq:*
- 4: /cgn2_6/ptodate/1/lna/6B.COMB.seq:*
- 5: /cgn2_6/ptodate/1/lna/H.COMB.seq:*
- 6: /cgn2_6/ptodate/1/lna/PC/US.COMB.seq:*
- 7: /cgn2_6/ptodate/1/lna/PP.COMB.seq:*
- 8: /cgn2_6/ptodate/1/lna/RE.COMB.seq:*
- 9: /cgn2_6/ptodate/1/lna/backfill.a1.seq:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Query Length | DB ID | Description |
|------------|-------|-------------|--------------|---------------------|---------------------|
| 1 | 486 | 10.2 | 2001 | US-09-799-451-695 | Sequence 695, App |
| 2 | 330.5 | 7.0 | 2387 | US-10-104-047-1902 | Sequence 1902, App |
| 3 | 330.5 | 7.0 | 2387 | US-10-104-047-1902 | Sequence 1902, App |
| 4 | 177 | 3.7 | 1434 | US-09-902-540-4356 | Sequence 4356, App |
| 5 | 177 | 3.7 | 23694 | US-09-902-540-1216 | Sequence 1216, App |
| 6 | 170.5 | 3.6 | 1827 | US-09-270-767-1308 | Sequence 1308, App |
| 7 | 170.5 | 3.6 | 1827 | US-09-270-767-16590 | Sequence 16590, App |
| 8 | 168.5 | 3.6 | 54033 | US-09-949-016-12091 | Sequence 12091, A |
| 9 | 167.5 | 3.5 | 5539 | US-09-949-016-14325 | Sequence 14325, A |
| 10 | 167 | 3.5 | 73519 | US-08-628-829-3 | Sequence 3, Appl1 |
| 11 | 167 | 3.5 | 10519 | US-09-949-016-16344 | Sequence 16344, A |
| 12 | 165.5 | 3.5 | 705 | US-09-270-767-1769 | Sequence 11769, A |
| 13 | 165.5 | 3.5 | 705 | US-09-270-767-5061 | Sequence 5061, Ap |
| 14 | 163 | 3.4 | 1835 | US-09-216-393B-80 | Sequence 20343, A |
| 15 | 163 | 3.4 | 4403765 | US-09-103-840A-2 | Sequence 80, Appl |
| 16 | 160.5 | 3.4 | 936 | US-09-270-767-4464 | Sequence 2, Appl1 |
| 17 | 160.5 | 3.4 | 936 | US-09-270-767-19746 | Sequence 4464, Ap |
| 18 | 158 | 3.3 | 98567 | US-09-949-016-11750 | Sequence 19746, A |
| 19 | 158 | 3.3 | 100567 | US-09-949-016-16934 | Sequence 11750, A |
| 20 | 158 | 3.3 | 194937 | US-09-949-016-17032 | Sequence 16934, A |
| 21 | 158 | 3.3 | 194937 | US-09-949-016-17032 | Sequence 17032, A |
| 22 | 157 | 3.3 | 276687 | US-09-949-016-13840 | Sequence 17033, A |
| 23 | 157 | 3.3 | 4411529 | US-09-103-840A-1 | Sequence 13840, A |
| 24 | 156.5 | 3.3 | 15651 | US-09-949-016-17349 | Sequence 1, Appl1 |
| 25 | 154.5 | 3.3 | 5253 | US-09-949-016-17349 | Sequence 17349, A |
| 26 | 154.5 | 3.3 | 390890 | US-09-949-016-14720 | Sequence 7, Appl1 |
| 27 | 154 | 3.2 | 851 | US-09-270-767-8286 | Sequence 14720, A |
| 28 | 154 | 3.2 | 851 | US-09-270-767-23568 | Sequence 8286, Ap |
| 29 | 154 | 3.2 | 43414 | US-09-949-016-12039 | Sequence 23568, Ap |
| 30 | 154 | 3.2 | 43415 | US-09-949-016-16491 | Sequence 12039, A |
| 31 | 153 | 3.2 | 226474 | US-09-949-016-13418 | Sequence 16491, A |
| 32 | 152 | 3.2 | 165651 | US-09-949-016-13032 | Sequence 13418, A |
| 33 | 151.5 | 3.2 | 177251 | US-09-949-016-15841 | Sequence 13032, A |
| 34 | 150.5 | 3.2 | 6789 | US-09-268-4460-43 | Sequence 15841, A |
| 35 | 150.5 | 3.2 | 90541 | US-09-758-359-3 | Sequence 43, Appl |
| 36 | 150.5 | 3.2 | 90541 | US-10-207-873-3 | Sequence 3, Appl1 |
| 37 | 150.5 | 3.2 | 767677 | US-09-949-016-12147 | Sequence 3, Appl1 |
| 38 | 150.5 | 3.2 | 767677 | US-09-949-016-17361 | Sequence 12147, A |
| 39 | 150 | 3.2 | 6644 | US-08-875-435B-5 | Sequence 17361, A |
| 40 | 149 | 3.1 | 268449 | US-09-949-016-17244 | Sequence 5, Appl1 |
| 41 | 148.5 | 3.1 | 5962 | US-08-931-999-4 | Sequence 17244, A |
| 42 | 148.5 | 3.1 | 6755 | US-09-949-016-14193 | Patent No. 5386025 |
| 43 | 148.5 | 3.1 | 247781 | US-09-949-016-14193 | Sequence 4, Appl1 |
| 44 | 147.5 | 3.1 | 3358 | US-09-902-540-528 | Sequence 14193, A |
| 45 | 147 | 3.1 | 1298 | US-08-948-705-3 | Sequence 528, App |

Search completed: December 4, 2005, 21:28:01
Job time : 3768 secs

OM protein - nucleotide search, using frame_plus_p2n model

Run on: December 4, 2005, 17:37:54 ; Search time 1464 Seconds
(without alignments)
5117.525 Million cell updates/sec

Title: US-10-792-307-4
Perfect score: 4744
Sequence: 1 MSHQYKGLKEARGVKGRV.....PSQTHPMASGASQAQPPH 906

Scoring table:

| | |
|---------------------------|---------------------------|
| BLOSUM62 | Xgapop 10.0 , Xgapext 0.5 |
| Xgapop 10.0 , Ygapext 0.5 | |
| Ygapop 6.0 , Fgapext 7.0 | |
| Delop 6.0 , Delext 7.0 | |

Searched: 9793542 .seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-XMODEL=frame+ p2n.model -DEV=k1p
-Q=/cgn2_1/USPTO_spool_p/US10792307/runat_23112005_080713_19227/app_query.fasta_1-1095
-DB=Published_Applications_NA_Main
-MINMATCH=0.1 -DOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1
-MATRIX=bl0sum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-HEAPSIZ=500 -MINLEN=0 -MODE=LOCAL -OUTFMT=ptc -NRM=ext
-USER=US10792307.gcgn.1.1549 @runat_23112005_080713_19227 -NCPU=6 -ICPU=3
-NO_JMAP -LARGEJURY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPEXT=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications_NA_Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Length | DB ID | Description |
|------------|--------|-------|--------|----------------------|------------------------------------|
| 1 | 4744 | 100.0 | 3169 | US-10-792-307-3 | Sequence 3, Appl |
| 2 | 4642 | 97.8 | 3121 | US-10-487-887-3 | Sequence 3, Appl |
| 3 | 4326.5 | 91.2 | 4895 | US-10-115-831-134 | Sequence 134, App |
| 4 | 4325.5 | 91.2 | 5027 | US-10-450-763-28100 | Sequence 28100, A |
| 5 | 3808 | 80.3 | 3216 | US-10-487-887-7 | Sequence 7, Appl |
| 6 | 3808 | 80.3 | 3216 | US-10-487-887-7 | Sequence 7, Appl |
| 7 | 2344.5 | 49.4 | 4333 | US-10-487-887-1 | Sequence 1, Appl |
| 8 | 2344.5 | 49.4 | 4333 | US-10-792-307-1 | Sequence 1, Appl |
| 9 | 2300 | 48.5 | 2895 | US-10-487-887-5 | Sequence 5, Appl |
| 10 | 2300 | 48.5 | 2895 | US-10-487-887-5 | Sequence 5, Appl |
| 11 | 1466 | 30.9 | 2560 | US-10-792-307-5 | Sequence 342, App |
| 12 | 1120.5 | 23.6 | 5929 | US-10-108-260A-342 | Sequence 342, App |
| 13 | 679 | 14.3 | 2738 | US-11-097-143-6038 | Sequence 6038, App |
| 14 | 517.5 | 10.9 | 2358 | US-10-108-260A-270 | Sequence 270, App |
| 15 | 515 | 10.9 | 2403 | US-09-965-529-73 | Sequence 13327, A |
| 16 | 515 | 10.9 | 2403 | US-09-965-529-73 | Sequence 73, Appl |
| 17 | 515 | 10.9 | 2403 | US-11-048-692-73 | Sequence 73, Appl |
| 18 | 499.5 | 10.5 | 2321 | US-09-374-046A-17 | Sequence 17, Appl |
| 19 | 499.5 | 10.5 | 2321 | US-10-616-263-17 | Sequence 17, Appl |
| 20 | 493 | 10.4 | 11963 | US-11-097-143-6037 | Sequence 6037, App |
| 21 | 486 | 10.2 | 2001 | US-10-302-172-695 | Sequence 695, App |
| 22 | 472.5 | 10.0 | 2629 | US-10-309-290-115 | Sequence 115, Appl |
| 23 | 463.5 | 9.8 | 4572 | US-10-495-148-61 | Sequence 61, Appl |
| 24 | 457.5 | 9.6 | 2902 | US-10-264-049-785 | Sequence 785, App |
| 25 | 449.5 | 9.5 | 2399 | US-10-108-260A-2102 | Sequence 2102, Ap |
| 26 | 449.5 | 9.5 | 3285 | US-10-487-752-2 | Sequence 2, Appl |
| 27 | 449.5 | 9.5 | 3285 | US-10-295-027-1150 | Sequence 1150, App |
| 28 | 447.5 | 9.4 | 2203 | US-10-309-290-113 | Sequence 113, App |
| 29 | 428.5 | 9.0 | 1839 | US-10-945-678-11 | Sequence 11, Appl |
| 30 | 422.5 | 8.9 | 2421 | US-10-487-752-11 | Sequence 11, Appl |
| 31 | 330.5 | 7.0 | 2387 | US-10-104-047-1902 | Sequence 1902, App |
| 32 | 328 | 6.9 | 1330 | US-10-945-678-6 | Sequence 6, Appl |
| 33 | 322.5 | 6.8 | 2452 | US-10-445-678-30 | Sequence 30, Appl |
| 34 | 322.5 | 6.8 | 2452 | US-10-445-678-30 | Sequence 10528, A |
| 35 | 298 | 6.3 | 2384 | US-10-108-260A-1066 | Sequence 1066, Ap |
| 36 | 287.5 | 6.3 | 1140 | US-10-264-237-220 | Sequence 120, App |
| 37 | 287.5 | 6.1 | 1060 | US-10-027-632-122322 | Sequence 122322, Sequence 120, App |
| 38 | 287.5 | 6.1 | 1060 | US-10-027-632-122322 | Sequence 122322, Sequence 120, App |
| 39 | 280.5 | 5.9 | 2290 | US-10-643-795A-11 | Sequence 11, Appl |
| 40 | 280.5 | 5.9 | 2290 | US-10-948-518-11 | Sequence 11, Appl |
| 41 | 250 | 5.3 | 600 | US-10-972-079-86723 | Sequence 86723, A |
| 42 | 245.5 | 5.2 | 1194 | US-10-357-930-22456 | Sequence 22456, A |
| 43 | 245.5 | 5.2 | 1194 | US-10-357-930-22456 | Sequence 22456, A |
| 44 | 245.5 | 5.2 | 1194 | US-10-357-930-28291 | Sequence 28291, A |
| 45 | 245 | 5.2 | 599 | US-10-972-079-86722 | Sequence 86722, A |

Search completed: December 4, 2005, 23:18:01
Job time : 1573 secs

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 20:26:42 ; Search time 231 Seconds

(without alignments)
1220.629 Million cell updates/sec

Title: US-10-792-307-4
Perfect score: 4744
Sequence: 1 MSHQKGLKEAKRGVGRV.....PSQTHPMSASGKSAQRPPI 906

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapact 0.5
Ygapop 10.0 , Ygapact 0.5
Fgapop 6.0 , Fgapact 7.0
Delop 6.0 , Delact 7.0

Searched: 3289935 seqs, 155610033 residues

Total number of hits satisfying chosen parameters: 6579870

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-1095
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnbn -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pcr -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=prco -NORMext -HEADSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10792307_0CGN_1_1_184_0runat_23112005_080714_19253
-NCPUG=6 -ICPU=3 -NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFBLCK=100
-LONGLOG -DEV.TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA_New: *
1: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq: *
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq: *
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq: *
4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq: *
5: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq: *
6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq: *
7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq: *
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2: *
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3: *

10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq: *
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query | | | | ID | Description |
|---------------|-------|-------|--------|----|---------------------|-------------------|
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| c 2 | 178.5 | 3.8 | 1611 | 6 | US-10-750-185-52663 | Sequence 52663, A |
| 3 | 178 | 3.8 | 1177 | 7 | US-11-102-240-129 | Sequence 129, App |
| 4 | 155.5 | 3.3 | 5468 | 6 | US-10-821-234-49 | Sequence 49, Appl |
| 5 | 154.5 | 3.3 | 5253 | 9 | US-11-004-057-3 | Sequence 3, Appl1 |
| 6 | 149.5 | 3.2 | 5233 | 7 | US-11-060-914-1 | Sequence 1, Appl1 |
| 7 | 144.5 | 3.0 | 5073 | 6 | US-10-908-125-827 | Sequence 827, App |
| 8 | 138.5 | 2.9 | 2492 | 6 | US-10-821-234-629 | Sequence 629, App |
| 9 | 137.5 | 2.9 | 177623 | 7 | US-11-112-908-41 | Sequence 41, Appl |
| 10 | 135.5 | 2.9 | 1359 | 6 | US-10-821-234-305 | Sequence 305, App |
| 11 | 135 | 2.8 | 150468 | 7 | US-11-112-908-56 | Sequence 56, Appl |
| 12 | 135 | 2.8 | 193789 | 7 | US-11-112-908-55 | Sequence 55, Appl |
| 13 | 126.5 | 2.7 | 161994 | 7 | US-11-112-908-57 | Sequence 57, Appl |
| 14 | 126 | 2.7 | 1132 | 7 | US-11-147-360-1 | Sequence 1, Appl1 |
| c 15 | 122.5 | 2.6 | 179892 | 7 | US-11-112-908-39 | Sequence 39, Appl |
| 16 | 122 | 2.6 | 1869 | 7 | US-11-147-360-3 | Sequence 3, Appl1 |
| 17 | 122 | 2.6 | 2031 | 7 | US-11-135-855-5 | Sequence 5, Appl1 |
| 18 | 122 | 2.6 | 2154 | 7 | US-11-135-855-6 | Sequence 6, Appl1 |
| 19 | 121 | 2.6 | 79528 | 6 | US-10-276-233A-6 | Sequence 6, Appl1 |
| 20 | 120 | 2.5 | 3513 | 6 | US-10-858-730-142 | Sequence 142, App |
| 21 | 120 | 2.5 | 6941 | 6 | US-10-432-483-49 | Sequence 49, Appl |
| 22 | 119.5 | 2.5 | 756 | 7 | US-11-135-855-15 | Sequence 15, Appl |
| 23 | 119.5 | 2.5 | 2158 | 6 | US-10-909-125-805 | Sequence 805, App |
| 24 | 119 | 2.5 | 2310 | 7 | US-11-073-579-1 | Sequence 1, Appl1 |
| 25 | 118.5 | 2.5 | 8424 | 6 | US-10-821-234-47 | Sequence 47, Appl |
| 26 | 117.5 | 2.5 | 1836 | 6 | US-10-467-657-3987 | Sequence 3987, Ap |
| c 27 | 117.5 | 2.5 | 3156 | 6 | US-10-467-657-3991 | Sequence 3991, Ap |
| 28 | 117 | 2.5 | 172147 | 7 | US-11-112-908-22 | Sequence 22, Appl |
| 29 | 117 | 2.5 | 188682 | 7 | US-11-112-908-23 | Sequence 23, Appl |
| 30 | 116 | 2.4 | 2129 | 6 | US-10-750-185-46845 | Sequence 46845, A |
| 31 | 116 | 2.4 | 2848 | 7 | US-11-060-914-3 | Sequence 3, Appl1 |
| 32 | 116 | 2.4 | 5212 | 6 | US-10-908-125-817 | Sequence 817, App |
| c 33 | 116 | 2.4 | 8631 | 6 | US-10-432-483-48 | Sequence 48, Appl |
| c 34 | 115.5 | 2.4 | 1619 | 6 | US-10-821-234-10 | Sequence 10, Appl |
| 35 | 115 | 2.4 | 3132 | 6 | US-10-392-234A-33 | Sequence 33, Appl |
| 36 | 115 | 2.4 | 159497 | 7 | US-11-112-908-61 | Sequence 61, Appl |
| 37 | 114.5 | 2.4 | 5946 | 6 | US-10-374-954-22 | Sequence 22, Appl |
| 38 | 114.5 | 2.4 | 5997 | 6 | US-10-374-954-20 | Sequence 20, Appl |
| 39 | 114.5 | 2.4 | 7027 | 6 | US-10-374-954-1 | Sequence 1, Appl1 |
| 40 | 114.5 | 2.4 | 7027 | 6 | US-10-374-954-3 | Sequence 3, Appl1 |
| c 41 | 114.5 | 2.4 | 157224 | 7 | US-11-112-908-51 | Sequence 51, Appl |
| c 42 | 114.5 | 2.4 | 159660 | 7 | US-11-112-908-43 | Sequence 43, Appl |
| c 43 | 114.5 | 2.4 | 170189 | 7 | US-11-112-908-50 | Sequence 50, Appl |
| 44 | 114 | 2.4 | 1377 | 6 | US-10-618-320A-2 | Sequence 2, Appl1 |
| c 45 | 114 | 2.4 | 3305 | 7 | US-11-017-550-68 | Sequence 68, Appl |

```
OM protein - nucleic search, using frame_plus_p2n model
Run on:      December 4, 2005, 17:37:51 ; Search time 7246 Seconds
              (without alignments)
              5850.000 Million cell updates/sec

Title:      US-10-792-307-4
Perfect score: 47/44
Sequence:    1 MSHQVKGKLEKENGKVGKRV.....PSQTHPWRSAKSKAKRPPH 906

Scoring table:
              BLOSUM62
              Xgapop 10.0 , Xgapext 0.5
              Ygapop 10.0 , Ygapext 0.5
              Fgapop 6.0 , Fgapext 7.0
              Delop  6.0 , Delext  7.0

Searched:    41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters:    8215650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_p/US10792307/runat_23112005_080712_19179/app_query.fasta_1
.1095
-DB=EST -QFMT=fastap -SUFFIX=p2n.rsc -MINMATCH=0.1 -LDOFCL=0 -LDOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blousum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORW=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10792307.RCGN.1.1.8010 @runat_23112005_080712_19179 -NCPU=6 -ICPU=3
-NO_MAP -LARGEOUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLDS
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
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          1: gb_est1:*
          2: gb_est2:*
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          4: gb_hic:*
          5: gb_est4:*
          6: gb_est5:*
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          8: gb_est7:*
          9: gb_gss1:*
          10: gb_gss2:*
          11: gb_gss3:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Job time : 7280 secs

SUMMARIES

| Result No. | Query | | | ID | Description |
|------------|-------|--------------|-------|----|-------------|
| | Score | Match Length | DB | | |
| 1 | 1682 | 35.5 | 11482 | 4 | BSM806678 |
| 2 | 973 | 20.5 | 1827 | 10 | AY406224 |
| 3 | 932 | 19.6 | 740 | 5 | BU262560 |
| 4 | 723 | 15.2 | 1827 | 10 | AY406226 |
| 5 | 670.5 | 14.1 | 822 | 11 | DQ030264 |
| 6 | 656 | 13.8 | 595 | 11 | DQ031957 |
| 7 | 652 | 13.7 | 1656 | 4 | AK016832 |
| 8 | 645 | 13.6 | 959 | 5 | BY716506 |
| 9 | 644 | 13.6 | 657 | 2 | BB614713 |
| 10 | 643 | 13.6 | 2435 | 4 | AK077146 |
| 11 | 628.5 | 13.2 | 633 | 10 | AY404862 |
| 12 | 625.5 | 13.2 | 822 | 11 | DQ030265 |
| 13 | 622.5 | 13.1 | 633 | 10 | AY404864 |
| 14 | 618 | 13.0 | 419 | 2 | BF544940 |
| 15 | 615 | 13.0 | 4496 | 4 | AK083189 |
| 16 | 599.5 | 12.6 | 633 | 10 | AY404863 |
| 17 | 591.5 | 12.5 | 4523 | 4 | CR933669 |
| 18 | 584 | 12.3 | 644 | 2 | BB624822 |
| 19 | 580 | 12.2 | 450 | 3 | BM482906 |
| 20 | 574 | 12.1 | 513 | 11 | DQ031958 |
| 21 | 571.5 | 12.0 | 1092 | 8 | DM708339 |
| 22 | 560 | 11.8 | 627 | 2 | BB617044 |
| 23 | 536 | 11.7 | 2708 | 4 | BC077431 |
| 24 | 538 | 11.3 | 676 | 1 | BB024587 |
| 25 | 530 | 11.2 | 829 | 9 | BB399926 |
| 26 | 519 | 10.9 | 2319 | 4 | CR605550 |
| 27 | 510.5 | 10.8 | 2204 | 4 | AK050105 |
| 28 | 508 | 10.7 | 876 | 9 | CC071886 |
| 29 | 508 | 10.7 | 1245 | 10 | CL641086 |
| 30 | 483 | 10.2 | 2721 | 4 | AK016573 |
| 31 | 463.5 | 9.8 | 3906 | 4 | AK028404 |
| 32 | 454.5 | 9.6 | 625 | 10 | BX144254 |
| 33 | 452.5 | 9.5 | 1171 | 10 | CL645372 |
| 34 | 452 | 9.5 | 583 | 3 | BP370498 |
| 35 | 449.5 | 9.3 | 2283 | 11 | DQ049496 |
| 36 | 439.5 | 9.2 | 790 | 7 | CK471553 |
| 37 | 435.5 | 9.1 | 3597 | 4 | CR749359 |
| 38 | 434 | 9.1 | 790 | 7 | CR853633 |
| 39 | 429 | 9.0 | 2866 | 4 | AK090179 |
| 40 | 416 | 8.8 | 247 | 6 | CD635963 |
| 41 | 416 | 8.8 | 247 | 6 | CD635964 |
| 42 | 411 | 8.7 | 2802 | 4 | AK077671 |
| 43 | 407 | 8.6 | 639 | 9 | BH376597 |
| 44 | 393 | 8.3 | 597 | 11 | DE054410 |
| 45 | 389 | 8.2 | 1648 | 11 | DQ046311 |

Search completed: December 4, 2005, 22:52:07